



#5

## SEQUENCE LISTING

<110> Mack, David H.  
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Eos Biotechnology, Inc.  
Case Western Reserve University

<120> Novel Methods of Diagnosis of Metastatic Colorectal Cancer, Compositions and Methods of Screening for Modulators of Metastatic Colorectal Cancer

<130> 018501-000840US

<140> US 10/087,080  
<141> 2002-02-27

<150> US 60/272,206  
<151> 2001-02-27

<150> US 60/281,149  
<151> 2001-04-02

<150> US 60/284,555  
<151> 2001-04-17

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<170> PatentIn Ver. 2.1

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 Leu Glu Val Cys Leu Leu Asn Ala Glu Asn Lys Val Val Asp Asn Gln  
 35 40 45  
  
 Ala Gly Thr Gln Gly Gln Leu Lys Val Leu Gly Ala Asn Leu Trp Trp  
 50 55 60

Pro Tyr Leu Met His Glu His Pro Ala Tyr Leu Tyr Ser Trp Glu Asp  
65 70 75 80

Gly Asp Cys Ser His Gln Ser Leu Gly Pro Leu Pro Ala Cys Asp Leu  
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Trp Asp Gln Leu His Leu Arg Ser Arg Gln Gly Gly Ser Val Cys Gly  
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35 40 45

Ala Gly Thr Gln Gly Gln Leu Lys Val Leu Gly Ala Asn Leu Trp Trp  
50 55 60

Pro Tyr Leu Met His Glu His Pro Ala Tyr Leu Tyr Ser Trp Glu Asp  
65 70 75 80

Gly Asp Cys Ser His Gln Ser Leu Gly Pro Leu Pro Ala Cys Asp Leu  
85 90 95

Cys Asp Gln Leu His Leu Arg Ser Arg Gln Gly Gly Ser Val Cys Gly  
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<223> n = q, a, c or t
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(SPP1)

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<212> PRT  
<213> Homo sapiens  
  
<220>  
<223> secreted phosphoprotein 1 (osteopontin, bone  
sialoprotein I, early T-lymphocyte activation 1)  
(SPP1)

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Tyr Asn Lys Tyr Pro Asp Ala Val Ala Thr Trp Leu Asn Pro Asp Pro  
           35                        40                        45  
  
 Ser Gln Lys Gln Asn Leu Leu Ala Pro Gln Thr Leu Pro Ser Lys Ser  
       50                        55                        60  
  
 Asn Glu Ser His Asp His Met Asp Asp Met Asp Asp Glu Asp Asp Asp  
    65                    70                        75                    80  
  
 Asp His Val Asp Ser Gln Asp Ser Ile Asp Ser Asn Asp Ser Asp Asp  
    85                    90                        95  
  
 Val Asp Asp Thr Asp Asp Ser His Gln Ser Asp Glu Ser His His Ser  
    100                    105                        110  
  
 Asp Glu Ser Asp Glu Leu Val Thr Asp Phe Pro Thr Asp Leu Pro Ala  
    115                    120                        125  
  
 Thr Glu Val Phe Thr Pro Val Val Pro Thr Val Asp Thr Tyr Asp Gly  
    130                    135                        140  
  
 Arg Gly Asp Ser Val Val Tyr Gly Leu Arg Ser Lys Ser Lys Lys Phe  
    145                    150                        155                    160  
  
 Arg Arg Pro Asp Ile Gln Tyr Pro Asp Ala Thr Asp Glu Asp Ile Thr  
    165                    170                        175  
  
 Ser His Met Glu Ser Glu Glu Leu Asn Gly Ala Tyr Lys Ala Ile Pro  
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 Val Ala Gln Asp Leu Asn Ala Pro Ser Asp Trp Asp Ser Arg Gly Lys  
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 Asp Ser Tyr Glu Thr Ser Gln Leu Asp Asp Gln Ser Ala Glu Thr His  
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 Ser His Lys Gln Ser Arg Leu Tyr Lys Arg Lys Ala Asn Asp Glu Ser  
    225                    230                        235                    240  
  
 Asn Glu His Ser Asp Val Ile Asp Ser Gln Glu Leu Ser Lys Val Ser  
    245                    250                        255  
  
 Arg Glu Phe His Ser His Glu Phe His Ser His Glu Asp Met Leu Val  
    260                    265                        270  
  
 Val Asp Pro Lys Ser Lys Glu Glu Asp Lys His Leu Lys Phe Arg Ile  
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 Ser His Glu Leu Asp Ser Ala Ser Ser Glu Val Asn  
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 <211> 3205  
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 <220>  
 <223> cadherin 3, type 1, P-cadherin (placental) (CDH3)

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<212> PRT

<213> Homo sapiens

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Cys Trp Leu Gln Cys Ala Ala Ser Glu Pro Cys Arg Ala Val Phe Arg  
   20              25              30

Glu Ala Glu Val Thr Leu Glu Ala Gly Gly Ala Glu Gln Glu Pro Gly  
   35              40              45

Gln Ala Leu Gly Lys Val Phe Met Gly Cys Pro Gly Gln Glu Pro Ala  
   50              55              60

Leu Phe Ser Thr Asp Asn Asp Asp Phe Thr Val Arg Asn Gly Glu Thr  
   65              70              75              80

Val Gln Glu Arg Arg Ser Leu Lys Glu Arg Asn Pro Leu Lys Ile Phe  
   85              90              95

Pro Ser Lys Arg Ile Leu Arg Arg His Lys Arg Asp Trp Val Val Ala  
   100             105             110

Pro Ile Ser Val Pro Glu Asn Gly Lys Gly Pro Phe Pro Gln Arg Leu  
   115             120             125

Asn Gln Leu Lys Ser Asn Lys Asp Arg Asp Thr Lys Ile Phe Tyr Ser  
   130             135             140

Ile Thr Gly Pro Gly Ala Asp Ser Pro Pro Glu Gly Val Phe Ala Val  
   145             150             155             160

Glu Lys Glu Thr Gly Trp Leu Leu Asn Lys Pro Leu Asp Arg Glu  
   165             170             175

Glu Ile Ala Lys Tyr Glu Leu Phe Gly His Ala Val Ser Glu Asn Gly  
   180             185             190

Ala Ser Val Glu Asp Pro Met Asn Ile Ser Ile Ile Val Thr Asp Gln  
   195             200             205

Asn Asp His Lys Pro Lys Phe Thr Gln Asp Thr Phe Arg Gly Ser Val  
   210             215             220

Leu Glu Gly Val Leu Pro Gly Thr Ser Val Met Gln Val Thr Ala Thr  
   225             230             235             240

Asp Glu Asp Asp Ala Ile Tyr Thr Tyr Asn Gly Val Val Ala Tyr Ser  
   245             250             255

Ile His Ser Gln Glu Pro Lys Asp Pro His Asp Leu Met Phe Thr Ile  
   260             265             270

His Arg Ser Thr Gly Thr Ile Ser Val Ile Ser Ser Gly Leu Asp Arg  
   275             280             285

Glu Lys Val Pro Glu Tyr Thr Leu Thr Ile Gln Ala Thr Asp Met Asp  
   290             295             300

Gly Asp Gly Ser Thr Thr Ala Val Ala Val Val Glu Ile Leu Asp  
 305                   310                   315                   320  
  
 Ala Asn Asp Asn Ala Pro Met Phe Asp Pro Gln Lys Tyr Glu Ala His  
 325                   330                   335  
  
 Val Pro Glu Asn Ala Val Gly His Glu Val Gln Arg Leu Thr Val Thr  
 340                   345                   350  
  
 Asp Leu Asp Ala Pro Asn Ser Pro Ala Trp Arg Ala Thr Tyr Leu Ile  
 355                   360                   365  
  
 Met Gly Gly Asp Asp Gly Asp His Phe Thr Ile Thr Thr His Pro Glu  
 370                   375                   380  
  
 Ser Asn Gln Gly Ile Leu Thr Thr Arg Lys Gly Leu Asp Phe Glu Ala  
 385                   390                   395                   400  
  
 Lys Asn Gln His Thr Leu Tyr Val Glu Val Thr Asn Glu Ala Pro Phe  
 405                   410                   415  
  
 Val Leu Lys Leu Pro Thr Ser Thr Ala Thr Ile Val Val His Val Glu  
 420                   425                   430  
  
 Asp Val Asn Glu Ala Pro Val Phe Val Pro Pro Ser Lys Val Val Glu  
 435                   440                   445  
  
 Val Gln Glu Gly Ile Pro Thr Gly Glu Pro Val Cys Val Tyr Thr Ala  
 450                   455                   460  
  
 Glu Asp Pro Asp Lys Glu Asn Gln Lys Ile Ser Tyr Arg Ile Leu Arg  
 465                   470                   475                   480  
  
 Asp Pro Ala Gly Trp Leu Ala Met Asp Pro Asp Ser Gly Gln Val Thr  
 485                   490                   495  
  
 Ala Val Gly Thr Leu Asp Arg Glu Asp Glu Gln Phe Val Arg Asn Asn  
 500                   505                   510  
  
 Ile Tyr Glu Val Met Val Leu Ala Met Asp Asn Gly Ser Pro Pro Thr  
 515                   520                   525  
  
 Thr Gly Thr Gly Thr Leu Leu Leu Thr Leu Ile Asp Val Asn Asp His  
 530                   535                   540  
  
 Gly Pro Val Pro Glu Pro Arg Gln Ile Thr Ile Cys Asn Gln Ser Pro  
 545                   550                   555                   560  
  
 Val Arg Gln Val Leu Asn Ile Thr Asp Lys Asp Leu Ser Pro His Thr  
 565                   570                   575  
  
 Ser Pro Phe Gln Ala Gln Leu Thr Asp Asp Ser Asp Ile Tyr Trp Thr  
 580                   585                   590  
  
 Ala Glu Val Asn Glu Glu Gly Asp Thr Val Val Leu Ser Leu Lys Lys  
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 Phe Leu Lys Gln Asp Thr Tyr Asp Val His Leu Ser Leu Ser Asp His  
 610                   615                   620

Gly Asn Lys Glu Gln Leu Thr Val Ile Arg Ala Thr Val Cys Asp Cys  
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 His Gly His Val Glu Thr Cys Pro Gly Pro Trp Lys Gly Gly Phe Ile  
 645 650 655  
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 660 665 670  
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 675 680 685  
 Leu Pro Glu Asp Asp Thr Arg Asp Asn Val Phe Tyr Tyr Gly Glu Glu  
 690 695 700  
 Gly Gly Gly Glu Glu Asp Gln Asp Tyr Asp Ile Thr Gln Leu His Arg  
 705 710 715 720  
 Gly Leu Glu Ala Arg Pro Glu Val Val Leu Arg Asn Asp Val Ala Pro  
 725 730 735  
 Thr Ile Ile Pro Thr Pro Met Tyr Arg Pro Arg Pro Ala Asn Pro Asp  
 740 745 750  
 Glu Ile Gly Asn Phe Ile Ile Glu Asn Leu Lys Ala Ala Asn Thr Asp  
 755 760 765  
 Pro Thr Ala Pro Pro Tyr Asp Thr Leu Leu Val Phe Asp Tyr Glu Gly  
 770 775 780  
 Ser Gly Ser Asp Ala Ala Ser Leu Ser Ser Leu Thr Ser Ser Ala Ser  
 785 790 795 800  
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<220>  
 <223> KIAA1199

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                  65                        70                        75                 80  
  
 Gly Lys Leu Val Ile Lys Asp His Asp Glu Pro Ile Val Leu Arg Thr  
                  85                        90                        95  
  
 Arg His Ile Leu Ile Asp Asn Gly Gly Glu Leu His Ala Gly Ser Ala  
                  100                       105                     110  
  
 Leu Cys Pro Phe Gln Gly Asn Phe Thr Ile Ile Leu Tyr Gly Arg Ala  
                  115                       120                     125  
  
 Asp Glu Gly Ile Gln Pro Asp Pro Tyr Tyr Gly Leu Lys Tyr Ile Gly  
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 Val Gly Lys Gly Gly Ala Leu Glu Leu His Gly Gln Lys Lys Leu Ser  
                  145                       150                     155                 160  
  
 Trp Thr Phe Leu Asn Lys Thr Leu His Pro Gly Gly Met Ala Glu Gly  
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 Gly Tyr Phe Phe Glu Arg Ser Trp Gly His Arg Gly Val Ile Val His  
                  180                       185                     190  
  
 Val Ile Asp Pro Lys Ser Gly Thr Val Ile His Ser Asp Arg Phe Asp  
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 Thr Tyr Arg Ser Lys Lys Glu Ser Glu Arg Leu Val Gln Tyr Leu Asn  
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 Ala Val Pro Asp Gly Arg Ile Leu Ser Val Ala Val Asn Asp Glu Gly  
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 Ser Arg Asn Leu Asp Asp Met Ala Arg Lys Ala Met Thr Lys Leu Gly  
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 Ser Lys His Phe Leu His Leu Gly Phe Arg His Pro Trp Ser Phe Leu  
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 Thr Val Lys Gly Asn Pro Ser Ser Val Glu Asp His Ile Glu Tyr  
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 His Gly His Arg Gly Ser Ala Ala Ala Arg Val Phe Lys Leu Phe Gln  
                  290                       295                     300  
  
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 Gln Asp Val Glu Trp Thr Glu Trp Phe Asp His Asp Lys Val Ser Gln  
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 Thr Lys Gly Gly Glu Lys Ile Ser Asp Leu Trp Lys Ala His Pro Gly  
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   385                         390                         395                         400  
  
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   405                         410                         415  
  
 Thr Asn Val Asn Ser Thr Ile Leu Asn Leu Glu Asp Asn Val Gln Ser  
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 Trp Lys Pro Gly Asp Thr Leu Val Ile Ala Ser Thr Asp Tyr Ser Met  
   435                         440                         445  
  
 Tyr Gln Ala Glu Glu Phe Gln Val Leu Pro Cys Arg Ser Cys Ala Pro  
   450                         455                         460  
  
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 Glu Ile Asp Gly Val Asp Met Arg Ala Glu Val Gly Leu Leu Ser Arg  
   485                         490                         495  
  
 Asn Ile Ile Val Met Gly Glu Met Glu Asp Lys Cys Tyr Pro Tyr Arg  
   500                         505                         510  
  
 Asn His Ile Cys Asn Phe Phe Asp Phe Asp Thr Phe Gly Gly His Ile  
   515                         520                         525  
  
 Lys Phe Ala Leu Gly Phe Lys Ala Ala His Leu Glu Gly Thr Glu Leu  
   530                         535                         540  
  
 Lys His Met Gly Gln Gln Leu Val Gly Gln Tyr Pro Ile His Phe His  
   545                         550                         555                         560  
  
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 Ile Arg Asp Leu Ser Ile His His Thr Phe Ser Arg Cys Val Thr Val  
   580                         585                         590  
  
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 Leu Gly His Cys Phe Phe Thr Glu Asp Gly Pro Glu Glu Arg Asn Thr  
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 Phe Asp His Cys Leu Gly Leu Leu Val Lys Ser Gly Thr Leu Leu Pro  
   625                         630                         635                         640  
  
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 Pro Gly Tyr Ile Pro Lys Pro Arg Gln Asp Cys Asn Ala Val Ser Thr  
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Phe Trp Met Ala Asn Pro Asn Asn Asn Leu Ile Asn Cys Ala Ala Ala  
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 Gly Ser Glu Glu Thr Gly Phe Trp Phe Ile Phe His His Val Pro Thr  
 690 695 700  
 Gly Pro Ser Val Gly Met Tyr Ser Pro Gly Tyr Ser Glu His Ile Pro  
 705 710 715 720  
 Leu Gly Lys Phe Tyr Asn Asn Arg Ala His Ser Asn Tyr Arg Ala Gly  
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 Met Ile Ile Asp Asn Gly Val Lys Thr Thr Glu Ala Ser Ala Lys Asp  
 740 745 750  
 Lys Arg Pro Phe Leu Ser Ile Ile Ser Ala Arg Tyr Ser Pro His Gln  
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 Met Met Asp Asn Arg Ile Trp Gly Pro Gly Gly Leu Asp His Ser Gly  
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 Arg Thr Leu Pro Ile Gly Gln Asn Phe Pro Ile Arg Gly Ile Gln Leu  
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 Tyr Asp Gly Pro Ile Asn Ile Gln Asn Cys Thr Phe Arg Lys Phe Val  
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 Ala Trp Gln Ser Cys Pro His Asn Asn Val Thr Gly Ile Ala Phe Glu  
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 Asp Val Pro Ile Thr Ser Arg Val Phe Phe Gly Glu Pro Gly Pro Trp  
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 Phe Asn Gln Leu Asp Met Asp Gly Asp Lys Thr Ser Val Phe His Asp  
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 Val Asp Gly Ser Val Ser Glu Tyr Pro Gly Ser Tyr Leu Thr Lys Asn  
 965 970 975  
 Asp Asn Trp Leu Val Arg His Pro Asp Cys Ile Asn Val Pro Asp Trp  
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Arg Gly Ala Ile Cys Ser Gly Cys Tyr Ala Gln Met Tyr Ile Gln Ala  
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 Tyr Lys Thr Ser Asn Leu Arg Met Lys Ile Ile Lys Asn Asp Phe Pro  
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 Ser His Pro Leu Tyr Leu Glu Gly Ala Leu Thr Arg Ser Thr His Tyr  
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 Gln Gln Tyr Gln Pro Val Val Thr Leu Gln Lys Gly Tyr Thr Ile His  
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 Trp Asp Gln Thr Ala Pro Ala Glu Leu Ala Ile Trp Leu Ile Asn Phe  
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 Ser Lys Thr Gly Val Phe Val Arg Thr Leu Gln Met Asp Lys Val Glu  
 1105 1110 1115 1120  
 Gln Ser Tyr Pro Gly Arg Ser His Tyr Tyr Trp Asp Glu Asp Ser Gly  
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 Pro Lys Asn Ala Gly Val Ser Asp Cys Thr Ala Thr Ala Tyr Pro Lys  
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 Ser Ser Lys Gln His Phe Phe His Leu Trp Asn Asp Phe Ala Tyr Ile  
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 Glu Val Asp Gly Lys Tyr Pro Ser Ser Glu Asp Gly Ile Gln Val  
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 Val Val Ile Asp Gly Asn Gln Gly Arg Val Val Ser His Thr Ser Phe  
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 Arg Asn Ser Ile Leu Gln Gly Ile Pro Trp Gln Leu Phe Asn Tyr Val  
 1265 1270 1275 1280  
 Ala Thr Ile Pro Asp Asn Ser Ile Val Leu Met Ala Ser Lys Gly Arg  
 1285 1290 1295  
 Tyr Val Ser Arg Gly Pro Trp Thr Arg Val Leu Glu Lys Leu Gly Ala  
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Asp Arg Gly Leu Lys Leu Lys Glu Gln Met Ala Phe Val Gly Phe Lys  
1315 1320 1325

Gly Ser Phe Arg Pro Ile Trp Val Thr Leu Asp Thr Glu Asp His Lys  
1330 1335 1340

Ala Lys Ile Phe Gln Val Val Pro Ile Pro Val Val Lys Lys Lys Lys  
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<211> 1619

<212> DNA

<213> Homo sapiens

<220>

<223> type I intermediate filament cytoketatin (HAIK1)

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<211> 422

<212> PRT

<213> Homo sapiens

<220>

<223> type I intermediate filament cytokeratin (HAIK1)

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                  35                     40                     45  
  
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                  50                     55                     60  
  
 Ser Pro Leu Leu Gly Gly Asn Gly Lys Ala Thr Met Gln Asn Leu Asn  
                  65                     70                     75                     80  
  
 Asp Arg Leu Ala Ser Tyr Leu Glu Lys Val Arg Ala Leu Glu Glu Ala  
                  85                     90                     95  
  
 Asn Met Lys Leu Glu Ser Arg Ile Leu Lys Trp His Gln Gln Arg Asp  
                  100                    105                     110  
  
 Pro Gly Ser Lys Lys Asp Tyr Ser Gln Tyr Glu Glu Asn Ile Thr His  
                  115                    120                     125  
  
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                  130                    135                     140  
  
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                  165                    170                     175  
  
 Gly Leu Arg Arg Thr Leu Asp Asn Leu Thr Ile Val Thr Thr Asp Leu  
                  180                    185                     190  
  
 Glu Gln Glu Val Glu Gly Met Arg Lys Glu Leu Ile Leu Met Lys Glu  
                  195                    200                     205  
  
 His His Glu Gln Glu Met Glu Glu His His Val Pro Ser Asp Phe Asn  
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 Arg Asp Leu Asp Thr Trp Tyr Lys Glu Gln Ser Ala Ala Met Ser Gln  
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 Glu Ala Ala Ser Pro Ala Thr Val Gln Ser Arg Gln Gly Asp Ile His  
                  275                    280                     285  
  
 Glu Leu Lys Arg Thr Phe Gln Ala Leu Glu Ile Asp Leu Gln Ala Gln  
                  290                    295                     300  
  
 Tyr Ser Thr Lys Ser Ala Leu Glu Asn Met Leu Ser Glu Thr Gln Ser  
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 Arg Tyr Ser Cys Lys Leu Gln Asp Met Gln Glu Ile Ile Ser His Tyr  
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Glu Glu Glu Leu Thr Gln Leu Arg His Glu Leu Glu Arg Gln Asn Asn  
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 Glu Tyr Gln Val Leu Leu Gly Ile Lys Thr His Leu Glu Lys Glu Ile  
           355                         360                         365  
  
 Thr Thr Tyr Arg Arg Leu Leu Glu Gly Glu Ser Glu Gly Thr Arg Glu  
           370                         375                         380  
  
 Glu Ser Lys Ser Ser Met Lys Val Ser Ala Thr Pro Lys Ile Lys Ala  
           385                         390                         395                         400  
  
 Ile Thr Gln Glu Thr Ile Asn Gly Arg Leu Val Leu Cys Gln Val Asn  
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gactcaaagg gaacatataaa atgtttccta tttttnnnnn nnnnnnnnnnnnnnnn 180
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tggcttgaa acttgcacag tctcatcatg tcaaacaagt gttgggttgc ccagggaaacg 180
caggcactgc ctgctctgaa aagatttcaa ataccgccat ctcaatcagt gaccacactg 240
cccttqctca attctqcaaa qqaqaqaaaa ttqaattttgt agttgttgaa ccagaacgcac 300

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 Glu Glu Ala Lys Lys Gly Leu Ala Ala Ile Lys Phe Glu Gly Ala Ile  
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Arg

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 Ala Val Asp Ile Met Phe Leu Leu Asp Gly Ser Asn Ser Val Gly Lys  
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 Gly Ser Phe Glu Arg Ser Lys His Phe Ala Ile Thr Val Cys Asp Gly  
 65 70 75 80  
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 85 90 95  
 Ser Thr Pro His Leu Glu Phe Pro Leu Asp Ser Phe Ser Thr Gln Gln  
 100 105 110  
 Glu Val Lys Ala Arg Ile Lys Arg Met Val Phe Lys Gly Gly Arg Thr  
 115 120 125  
 Glu Thr Glu Leu Ala Leu Lys Tyr Leu Leu His Arg Gly Leu Pro Gly  
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 Gly Arg Asn Ala Ser Val Pro Gln Ile Leu Ile Ile Val Thr Asp Gly  
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 Lys Ser Gln Gly Asp Val Ala Leu Pro Ser Lys Gln Leu Lys Glu Arg  
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 Gly Val Thr Val Phe Ala Val Gly Val Arg Phe Pro Arg Trp Glu Glu  
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 195 200 205  
 Glu Gln Val Glu Asp Ala Thr Asn Gly Leu Phe Ser Thr Leu Ser Ser  
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 Pro Cys Glu His Arg Thr Leu Glu Met Val Arg Glu Phe Ala Gly Asn  
 245 250 255  
 Ala Pro Cys Trp Arg Gly Ser Arg Arg Thr Leu Ala Val Leu Ala Ala  
 260 265 270  
 His Cys Pro Phe Tyr Ser Trp Lys Arg Val Phe Leu Thr His Pro Ala  
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 Thr Cys Tyr Arg Thr Thr Cys Pro Gly Pro Cys Asp Ser Gln Pro Cys  
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 Gln Asn Gly Gly Thr Cys Val Pro Glu Gly Leu Asp Gly Tyr Gln Cys  
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Leu Cys Pro Leu Ala Phe Gly Gly Glu Ala Asn Cys Ala Leu Lys Leu  
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 Gln Asp Val Pro Asp Leu Val Trp Ser Leu Asp Gly Ile Pro Phe Arg  
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                   595                     600                     605  
  
 Ser Ala Gly Thr Ala Leu Leu His Ile Tyr Asp Lys Val Met Thr Val  
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 Gln Arg Gly Ala Arg Pro Gly Val Pro Lys Ala Val Val Val Leu Thr  
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Gly Gly Arg Gly Ala Glu Asp Ala Ala Val Pro Ala Gln Lys Leu Arg  
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 Asn Asn Gly Ile Ser Val Leu Val Val Gly Val Gly Pro Val Leu Ser  
 660 665 670  
 Glu Gly Leu Arg Arg Leu Ala Gly Pro Arg Asp Ser Leu Ile His Val  
 675 680 685  
 Ala Ala Tyr Ala Asp Leu Arg Tyr His Gln Asp Val Leu Ile Glu Trp  
 690 695 700  
 Leu Cys Gly Glu Ala Lys Gln Pro Val Asn Leu Cys Lys Pro Ser Pro  
 705 710 715 720  
 Cys Met Asn Glu Gly Ser Cys Val Leu Gln Asn Gly Ser Tyr Arg Cys  
 725 730 735  
 Lys Cys Arg Asp Gly Trp Glu Gly Pro His Cys Glu Asn Arg Glu Trp  
 740 745 750  
 Ser Ser Cys Ser Val Cys Val Ser Gln Gly Trp Ile Leu Glu Thr Pro  
 755 760 765  
 Leu Arg His Met Ala Pro Val Gln Glu Gly Ser Ser Arg Thr Pro Pro  
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<213> Homo sapiens
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 Phe Asn Tyr Ile Glu Lys Leu Lys Tyr Glu His His Leu Lys Glu Ser  
                   165                     170                     175  
  
 Leu Lys Gln Met Asn Val Gly Glu Asp Leu Glu Asn Glu Asp Phe Asp  
                   180                     185                     190  
  
 Ser Arg Arg Tyr Lys Phe Leu Asp Asp Asp Gly Ser Ile Ser Pro Ile  
                   195                     200                     205  
  
 Glu Glu Ser Thr Ala Glu Asp Glu Asp Ala Thr His Leu Glu Asp Asn  
                   210                     215                     220  
  
 Glu Cys Asp Ile Lys Leu Ala Gly Asp Ser Phe Ile Val Ser Ser Glu  
                   225                     230                     235                     240  
  
 Phe Pro Val Arg Leu Ser Val Tyr Leu Glu Glu Asp Ile Thr Glu  
                   245                     250                     255  
  
 Glu Ala Ala Leu Ser Lys Lys Arg Ala Thr Lys Ala Lys Asn Thr Gly  
                   260                     265                     270  
  
 Gln Arg Gly Leu Lys Met  
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<210> 27  
 <211> 2336  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <223> FLJ23363, clone HEP15507

<400> 27

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 ccgaggcctg ggttacaagc agcaagtgcg cggttggggc cactgcgagg ccgttttaga 180  
 aaactgttta aaacaaagag caattgtatgg ataaatcagg aatagattct cttgaccatg 240  
 tgacatctga tgctgtggaa cttgcaaatc gaagtgataa ctcttctgtat agcagctt 300  
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 ttgttcgtac acctgaaagt gttcacgca gtgattcatc aagtgactca tcttttgaac 420  
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 aaaaaaaagaa aaagaggagg taccagccaa cagaagacc acgggaaaga ccagaaggaa 540  
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 gcttcccatt tttagaatca gagaatggaa aaaacgcacc ttggagaaaa attttaacgt 660  
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 acctgaaaga atcattgaag caaatgaatg ttgttgaaga tttagaaaat gaagattttg 780  
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 gatcatttc attaaaaagg tatgtatca tttagaaaaga cattttatg ggtcatttca 1860  
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 cttaaataa ttttgtctaa tgctacatat acacaattaa aaaaccttta cactatttct 2220  
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<210> 28  
 <211> 278  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> FLJ23363, clone HEP15507, MGC5306

<400> 28  
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 20 25 30  
 Lys Thr Gln Cys Ile Pro Tyr Ser Pro Lys Gly Glu Lys Arg Asn Pro  
 35 40 45

Ile Arg Lys Phe Val Arg Thr Pro Glu Ser Val His Ala Ser Asp Ser  
 50 55 60

Ser Ser Asp Ser Ser Phe Glu Pro Ile Pro Leu Thr Ile Lys Ala Ile  
 65 70 75 80

Phe Glu Arg Phe Lys Asn Arg Lys Lys Arg Tyr Lys Lys Lys Lys Lys  
 85 90 95

Arg Arg Tyr Gln Pro Thr Gly Arg Pro Arg Gly Arg Pro Glu Gly Arg  
 100 105 110

Arg Asn Pro Ile Tyr Ser Leu Ile Asp Lys Lys Lys Gln Phe Arg Ser  
 115 120 125

Arg Gly Ser Gly Phe Pro Phe Leu Glu Ser Glu Asn Glu Lys Asn Ala  
 130 135 140

Pro Trp Arg Lys Ile Leu Thr Phe Glu Gln Ala Val Ala Arg Gly Phe  
 145 150 155 160

Phe Asn Tyr Ile Glu Lys Leu Lys Tyr Glu His His Leu Lys Glu Ser  
 165 170 175

Leu Lys Gln Met Asn Val Gly Glu Asp Leu Glu Asn Glu Asp Phe Asp  
 180 185 190

Ser Arg Arg Tyr Lys Phe Leu Asp Asp Asp Gly Ser Ile Ser Pro Ile  
 195 200 205

Glu Glu Ser Thr Ala Glu Asp Glu Asp Ala Thr His Leu Glu Asp Asn  
 210 215 220

Glu Cys Asp Ile Lys Leu Ala Gly Asp Ser Phe Ile Val Ser Ser Glu  
 225 230 235 240

Phe Pro Val Arg Leu Ser Val Tyr Leu Glu Glu Asp Ile Thr Glu  
 245 250 255

Glu Ala Ala Leu Ser Lys Lys Arg Ala Thr Lys Ala Lys Asn Thr Gly  
 260 265 270

Gln Arg Gly Leu Lys Met  
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<210> 29  
 <211> 2174  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> nuclear factor (erythroid-derived 2)-like 3  
 (NFE2L3)

<400> 29  
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 gagaaggcac ccgcggAACc gacggctca gttggccggacg ctggcggatg tgccgagcgag 180  
 gagaatgggg tactaagaga aaagcaccaa gctgtggatc atagttccca gcatgaggaa 240  
 aatgaagaaa gggtgtcagc ccagaaggag aactcacttc agcagaatga tggatgatgaa 300

aacaaaatag cagagaaacc tgactggag gcagaaaaaaga ccactgaatc tagaaatgag 360  
 agacatctga atggacaga tacttcttc tctctggaaag acttattcca gttgcttca 420  
 tcacagcctg aaaattcaact ggagggcatc tcattggag atattcctct tccaggcagt 480  
 atcagtgtatc gcatgaattc ttcagcacat tatacatgtaa acttcagcca ggctataagt 540  
 caggatgtga atcttcatga ggccatcttg ctttgtccca acaatacatt tagaagagat 600  
 ccaacagcaa ggacttcaca gtcacaagaa ccattctgc agttaaattc tcataccacc 660  
 aatcctgagc aaacccttcc tggaaactaat ttgacaggat ttcttcacc gggtgacaat 720  
 catatgagga atctaacaag ccaagaccta ctgtatgacc ttgacataaa tatattttagt 780  
 gagataaact taatgtcatt ggccacagaa gacaactttg atccaatcga tgtttctcag 840  
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 acagatagaa acttgagccg ttagaacacg cgtgctaaag ctttgcataat cccttttct 1260  
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 gctgcgcaga actgtcgtaa acgcaaattt gacataattt tgaattttaga agatgtatgt 1440  
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 attaacataa tggaaacagaa actgcatgac ctttatcatg atatttttag tagattaaga 1560  
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 ctgctacttg aataactcg ttaacgctgt tttgaagctt acatggacaa atgttttagga 1860  
 cttcaagatc acacttgcgtt gcaatctggg ggagccacaa ctttgcataat agtgcattgt 1920  
 atacaaaatt catagttatc tccaaagaat aggttaacat gaaaacccag taagactttc 1980  
 catcttggca gccatccccc ttaagagta gttggttact tcaaaaagag caaacactgg 2040  
 ggatcaaattt attttaagag gtatttcagt tttaaatgca aaatagccctt attttcattt 2100  
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 aaattttgtt ttct 2174

<210> 30  
 <211> 400  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> nuclear factor (erythroid-derived 2)-like 3  
 (NFE2L3)

<400> 30  
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Gln Asp Val Asn Leu His Glu Ala Ile Leu Leu Cys Pro Asn Asn Thr  
 20 25 30

Phe Arg Arg Asp Pro Thr Ala Arg Thr Ser Gln Ser Gln Glu Pro Phe  
 35 40 45

Leu Gln Leu Asn Ser His Thr Thr Asn Pro Glu Gln Thr Leu Pro Gly  
 50 55 60

Thr Asn Leu Thr Gly Phe Leu Ser Pro Val Asp Asn His Met Arg Asn  
 65 70 75 80

Leu Thr Ser Gln Asp Leu Leu Tyr Asp Leu Asp Ile Asn Ile Phe Asp  
 85 90 95

Glu Ile Asn Leu Met Ser Leu Ala Thr Glu Asp Asn Phe Asp Pro Ile  
                  100                         105                         110  
  
 Asp Val Ser Gln Leu Phe Asp Glu Pro Asp Ser Asp Ser Gly Leu Ser  
                  115                         120                         125  
  
 Leu Asp Ser Ser His Asn Asn Thr Ser Val Ile Lys Ser Asn Ser Ser  
                  130                         135                         140  
  
 His Ser Val Cys Asp Glu Gly Ala Ile Gly Tyr Cys Thr Asp His Glu  
                  145                         150                         155                         160  
  
 Ser Ser Ser His His Asp Leu Glu Gly Ala Val Gly Gly Tyr Tyr Pro  
                  165                         170                         175  
  
 Glu Pro Ser Lys Leu Cys His Leu Asp Gln Ser Asp Ser Asp Phe His  
                  180                         185                         190  
  
 Gly Asp Leu Thr Phe Gln His Val Phe His Asn His Thr Tyr His Leu  
                  195                         200                         205  
  
 Gln Pro Thr Ala Pro Glu Ser Thr Ser Glu Pro Phe Pro Trp Pro Gly  
                  210                         215                         220  
  
 Lys Ser Gln Lys Ile Arg Ser Arg Tyr Leu Glu Asp Thr Asp Arg Asn  
                  225                         230                         235                         240  
  
 Leu Ser Arg Asp Glu Gln Arg Ala Lys Ala Leu His Ile Pro Phe Ser  
                  245                         250                         255  
  
 Val Asp Glu Ile Val Gly Met Pro Val Asp Ser Phe Asn Ser Met Leu  
                  260                         265                         270  
  
 Ser Arg Tyr Tyr Leu Thr Asp Leu Gln Val Ser Leu Ile Arg Asp Ile  
                  275                         280                         285  
  
 Arg Arg Arg Gly Lys Asn Lys Val Ala Ala Gln Asn Cys Arg Lys Arg  
                  290                         295                         300  
  
 Lys Leu Asp Ile Ile Leu Asn Leu Glu Asp Asp Val Cys Asn Leu Gln  
                  305                         310                         315                         320  
  
 Ala Lys Lys Glu Thr Leu Lys Arg Glu Gln Ala Gln Cys Asn Lys Ala  
                  325                         330                         335  
  
 Ile Asn Ile Met Lys Gln Lys Leu His Asp Leu Tyr His Asp Ile Phe  
                  340                         345                         350  
  
 Ser Arg Leu Arg Asp Asp Gln Gly Arg Pro Val Asn Pro Asn His Tyr  
                  355                         360                         365  
  
 Ala Leu Gln Cys Thr His Asp Gly Ser Ile Leu Ile Val Pro Lys Glu  
                  370                         375                         380  
  
 Leu Val Ala Ser Gly His Lys Lys Glu Thr Gln Lys Gly Lys Arg Lys  
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<210> 31
<211> 1209
<212> DNA
<213> Homo sapiens

<220>
<223> winged helix/forkhead transcription factor (HFH1)

<220>
<221> modified_base
<222> (1161)
<223> n = g, a, c or t

<400> 31
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ggctcagatg gggactgcgc ggccaagccg tccgcggcgg gccgcgccag agatacgcag 180
ggcgcacggcg aacagagtgc gggaggcggg cggggcgcgg aggaggcgt cccggcagca 240
gctgctgcag cgggtgtggc ggagggcgcg gaggccggg cggcggggcc aggccgcggc 300
ggcgcgggga gcccgcgggg tgacgcgc aagccatata cgcggcggcc caagcccccc 360
tactcgtaa tcgcgtcat cgccatggcc atccgcact cggcggcgg ggcgttgacg 420
ctggcggaga tcaacgagta cctcatggc aagttccct tttccgcgg cagctacacg 480
ggctggcgca actccgtgcg ccacaacctt tcgctcaacg actgcttcgt caaggtgctg 540
cgcgaccctt cgcggccctg gggcaaggac aactactgga tgctcaaccc caacagcgcag 600
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ctccgaggcc cggcggccgg cggcgcgcac ctgtactgcc ccctgcggct gcccgcagcc 1140
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ctagcttga 1209

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<210> 32
<211> 402
<212> PRT
<213> Homo sapiens

<220>
<223> winged helix/forkhead transcription factor (HFH1)

<400> 32
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Gly Ser Asp Leu Glu Gly Ala Gly Gly Ser Asp Ala Pro Ser Pro Leu
    20          25          30

Ser Ala Ala Gly Asp Asp Ser Leu Gly Ser Asp Gly Asp Cys Ala Ala
    35          40          45

Lys Pro Ser Ala Gly Gly Ala Arg Asp Thr Gln Gly Asp Gly Glu
    50          55          60

Gln Ser Ala Gly Gly Pro Gly Ala Glu Glu Ala Ile Pro Ala Ala
    65          70          75          80

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Ala Ala Ala Ala Val Val Ala Glu Gly Ala Glu Ala Gly Ala Ala Gly  
 85 90 95

Pro Gly Ala Gly Gly Ala Gly Ser Gly Glu Gly Ala Arg Ser Lys Pro  
 100 105 110

Tyr Thr Arg Arg Pro Lys Pro Pro Tyr Ser Tyr Ile Ala Leu Ile Ala  
 115 120 125

Met Ala Ile Arg Asp Ser Ala Gly Gly Arg Leu Thr Leu Ala Glu Ile  
 130 135 140

Asn Glu Tyr Leu Met Gly Lys Phe Pro Phe Phe Arg Gly Ser Tyr Thr  
 145 150 155 160

Gly Trp Arg Asn Ser Val Arg His Asn Leu Ser Leu Asn Asp Cys Phe  
 165 170 175

Val Lys Val Leu Arg Asp Pro Ser Arg Pro Trp Gly Lys Asp Asn Tyr  
 180 185 190

Trp Met Leu Asn Pro Asn Ser Glu Tyr Thr Phe Ala Asp Gly Val Phe  
 195 200 205

Arg Arg Arg Arg Lys Arg Leu Ser His Arg Ala Pro Val Pro Ala Pro  
 210 215 220

Gly Leu Arg Pro Glu Glu Ala Pro Gly Leu Pro Ala Ala Pro Pro Pro  
 225 230 235 240

Ala Pro Ala Ala Pro Ala Ser Pro Arg Met Arg Ser Pro Ala Arg Gln  
 245 250 255

Glu Glu Arg Ala Ser Pro Ala Gly Lys Phe Ser Ser Ser Phe Ala Ile  
 260 265 270

Asp Ser Ile Leu Arg Lys Pro Phe Arg Ser Arg Arg Leu Arg Asp Thr  
 275 280 285

Ala Pro Gly Thr Thr Leu Gln Trp Gly Ala Ala Pro Cys Pro Pro Leu  
 290 295 300

Pro Ala Phe Pro Ala Leu Leu Pro Ala Ala Pro Cys Arg Ala Leu Leu  
 305 310 315 320

Pro Leu Cys Ala Tyr Gly Ala Gly Glu Pro Ala Arg Leu Gly Ala Arg  
 325 330 335

Glu Ala Glu Val Pro Pro Thr Ala Pro Pro Leu Leu Leu Ala Pro Leu  
 340 345 350

Pro Ala Ala Ala Pro Ala Lys Pro Leu Arg Gly Pro Ala Ala Gly Gly  
 355 360 365

Ala His Leu Tyr Cys Pro Leu Arg Leu Pro Ala Ala Leu Gln Ala Ala  
 370 375 380

Leu Val Arg Arg Pro Gly Pro His Leu Ser Tyr Pro Val Glu Thr Leu  
 385 390 395 400

Leu Ala

<210> 33  
 <211> 3218  
 <212> DNA  
 <213> Homo sapiens  
  
 <220>  
 <223> chloride channel, calcium activatd, family member  
     4 (CLCA4)

<400> 33  
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 aataataatg gctttaaga tattgtcatt gttatagatc ctatgtgcc agaagatgaa 180  
 aaaataattg aacaaataga ggatatggtg actacagctt ctacgtacct gtttgaagcc 240  
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 ccacctacac tcccaggtag agatgaacca tacaccaagc agttcacaga atgtggagag 420  
 aaaggcgaat acattcactt caccctgac cttctacttg gaaaaaaaaaca aaatgaatat 480  
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 agtagagcat gcagaattga ttctacaaca aaactgtatg gaaaagattt tcaattctt 720  
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<211> 917  
<212> PRT  
<213> Homo sapiens

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20 25 30  
  
Asp Ile Val Ile Val Ile Asp Pro Ser Val Pro Glu Asp Glu Lys Ile  
35 40 45  
  
Ile Glu Gln Ile Glu Asp Met Val Thr Thr Ala Ser Thr Tyr Leu Phe  
50 55 60  
  
Glu Ala Thr Glu Lys Arg Phe Phe Lys Asn Val Ser Ile Leu Ile  
65 70 75 80  
  
Pro Glu Asn Trp Lys Glu Asn Pro Gln Tyr Lys Arg Pro Lys His Glu  
85 90 95  
  
Asn His Lys His Ala Asp Val Ile Val Ala Pro Pro Thr Leu Pro Gly  
100 105 110  
  
Arg Asp Glu Pro Tyr Thr Lys Gln Phe Thr Glu Cys Gly Glu Lys Gly  
115 120 125  
  
Glu Tyr Ile His Phe Thr Pro Asp Leu Leu Gly Lys Lys Gln Asn  
130 135 140  
  
Glu Tyr Gly Pro Pro Gly Lys Leu Phe Val His Glu Trp Ala His Leu  
145 150 155 160  
  
Arg Trp Gly Val Phe Asp Glu Tyr Asn Glu Asp Gln Pro Phe Tyr Arg  
165 170 175  
  
Ala Lys Ser Lys Lys Ile Glu Ala Thr Arg Cys Ser Ala Gly Ile Ser  
180 185 190  
  
Gly Arg Asn Arg Val Tyr Lys Cys Gln Gly Gly Ser Cys Leu Ser Arg  
195 200 205  
  
Ala Cys Arg Ile Asp Ser Thr Thr Lys Leu Tyr Gly Lys Asp Cys Gln  
210 215 220  
  
Phe Phe Pro Asp Lys Val Gln Thr Glu Lys Ala Ser Ile Met Phe Met  
225 230 235 240

Gln Ser Ile Asp Ser Val Val Glu Phe Cys Asn Glu Lys Thr His Asn  
                  245                     250                     255  
  
 Gln Glu Ala Pro Ser Leu Gln Asn Ile Lys Cys Asn Phe Arg Ser Thr  
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 Trp Glu Val Ile Ser Asn Ser Glu Asp Phe Lys Asn Thr Ile Pro Met  
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 Val Thr Pro Pro Pro Pro Val Phe Ser Leu Leu Lys Ile Arg Gln  
                  290                     295                     300  
  
 Arg Ile Val Cys Leu Val Leu Asp Lys Ser Gly Ser Met Gly Gly Lys  
                  305                     310                     315                     320  
  
 Asp Arg Leu Asn Arg Met Asn Gln Ala Ala Lys His Phe Leu Leu Gln  
                  325                     330                     335  
  
 Thr Val Glu Asn Gly Ser Trp Val Gly Met Val His Phe Asp Ser Thr  
                  340                     345                     350  
  
 Ala Thr Ile Val Asn Lys Leu Ile Gln Ile Lys Ser Ser Asp Glu Arg  
                  355                     360                     365  
  
 Asn Thr Leu Met Ala Gly Leu Pro Thr Tyr Pro Leu Gly Gly Thr Ser  
                  370                     375                     380  
  
 Ile Cys Ser Gly Ile Lys Tyr Ala Phe Gln Val Ile Gly Glu Leu His  
                  385                     390                     395                     400  
  
 Ser Gln Leu Asp Gly Ser Glu Val Leu Leu Leu Thr Asp Gly Glu Asp  
                  405                     410                     415  
  
 Asn Thr Ala Ser Ser Cys Ile Asp Glu Val Lys Gln Ser Gly Ala Ile  
                  420                     425                     430  
  
 Val His Phe Ile Ala Leu Gly Arg Ala Ala Asp Glu Ala Val Ile Glu  
                  435                     440                     445  
  
 Met Ser Lys Ile Thr Gly Gly Ser His Phe Tyr Val Ser Asp Glu Ala  
                  450                     455                     460  
  
 Gln Asn Asn Gly Leu Ile Asp Ala Phe Gly Ala Leu Thr Ser Gly Asn  
                  465                     470                     475                     480  
  
 Thr Asp Leu Ser Gln Lys Ser Leu Gln Leu Glu Ser Lys Gly Leu Thr  
                  485                     490                     495  
  
 Leu Asn Ser Asn Ala Trp Met Asn Asp Thr Val Ile Ile Asp Ser Thr  
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 Val Gly Lys Asp Thr Phe Phe Leu Ile Thr Trp Asn Ser Leu Pro Pro  
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 Ser Ile Ser Leu Trp Asp Pro Ser Gly Thr Ile Met Glu Asn Phe Thr  
                  530                     535                     540  
  
 Val Asp Ala Thr Ser Lys Met Ala Tyr Leu Ser Ile Pro Gly Thr Ala  
                  545                     550                     555                     560

Lys Val Gly Thr Trp Ala Tyr Asn Leu Gln Ala Lys Ala Asn Pro Glu  
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Thr Leu Thr Ile Thr Val Thr Ser Arg Ala Ala Asn Ser Ser Val Pro  
580 585 590

Pro Ile Thr Val Asn Ala Lys Met Asn Lys Asp Val Asn Ser Phe Pro  
595 600 605

Ser Pro Met Ile Val Tyr Ala Glu Ile Leu Gln Gly Tyr Val Pro Val  
610 615 620

Leu Gly Ala Asn Val Thr Ala Phe Ile Glu Ser Gln Asn Gly His Thr  
625 630 635 640

Glu Val Leu Glu Leu Leu Asp Asn Gly Ala Gly Ala Asp Ser Phe Lys  
645 650 655

Asn Asp Gly Val Tyr Ser Arg Tyr Phe Thr Ala Tyr Thr Glu Asn Gly  
660 665 670

Arg Tyr Ser Leu Lys Val Arg Ala His Gly Gly Ala Asn Thr Ala Arg  
675 680 685

Leu Lys Leu Arg Pro Pro Leu Asn Arg Ala Ala Tyr Ile Pro Gly Trp  
690 695 700

Val Val Asn Gly Glu Ile Glu Ala Asn Pro Pro Arg Pro Glu Ile Asp  
705 710 715 720

Glu Asp Thr Gln Thr Thr Leu Glu Asp Phe Ser Arg Thr Ala Ser Gly  
725 730 735

Gly Ala Phe Val Val Ser Gln Val Pro Ser Leu Pro Leu Pro Asp Gln  
740 745 750

Tyr Pro Pro Ser Gln Ile Thr Asp Leu Asp Ala Thr Val His Glu Asp  
755 760 765

Lys Ile Ile Leu Thr Trp Thr Ala Pro Gly Asp Asn Phe Asp Val Gly  
770 775 780

Lys Val Gln Arg Tyr Ile Ile Arg Ile Ser Ala Ser Ile Leu Asp Leu  
785 790 795 800

Arg Asp Ser Phe Asp Asp Ala Leu Gln Val Asn Thr Thr Asp Leu Ser  
805 810 815

Pro Lys Glu Ala Asn Ser Lys Glu Ser Phe Ala Phe Lys Pro Glu Asn  
820 825 830

Ile Ser Glu Glu Asn Ala Thr His Ile Phe Ile Ala Ile Lys Ser Ile  
835 840 845

Asp Lys Ser Asn Leu Thr Ser Lys Val Ser Asn Ile Ala Gln Val Thr  
850 855 860

Leu Phe Ile Pro Gln Ala Asn Pro Asp Asp Ile Asp Pro Thr Pro Thr  
865 870 875 880

Pro Thr Pro Thr Pro Asp Lys Ser His Asn Ser Gly Val Asn Ile Ser  
885 890 895

Thr Leu Val Leu Ser Val Ile Gly Ser Val Val Ile Val Asn Phe Ile  
900 905 910

Leu Ser Thr Thr Ile  
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<211> 5749

<212> DNA

<213> Homo sapiens

<220>

<223> nuclear receptor subfamily 3, group C, member 2  
(NR3C2)

<400> 35

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gtagacggcg agagacggac cccggccgag gcagggatgg agaccaaagg ctaccacagt 240  
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 <211> 984  
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 <213> Homo sapiens

<220>

<223> nuclear receptor subfamily 3, group C, member 2  
(NR3C2)

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20 25 30  
Pro Thr Glu Arg Thr Asp Glu Asn Asn Tyr Met Glu Ile Val Asn Val  
35 40 45  
Ser Cys Val Ser Gly Ala Ile Pro Asn Asn Ser Thr Gln Gly Ser Ser  
50 55 60  
Lys Glu Lys Gln Glu Leu Leu Pro Cys Leu Gln Gln Asp Asn Asn Arg  
65 70 75 80  
Pro Gly Ile Leu Thr Ser Asp Ile Lys Thr Glu Leu Glu Ser Lys Glu  
85 90 95  
Leu Ser Ala Thr Val Ala Glu Ser Met Gly Leu Tyr Met Asp Ser Val  
100 105 110  
Arg Asp Ala Asp Tyr Ser Tyr Glu Gln Gln Asn Gln Gln Gly Ser Met  
115 120 125  
Ser Pro Ala Lys Ile Tyr Gln Asn Val Glu Gln Leu Val Lys Phe Tyr  
130 135 140  
Lys Gly Asn Gly His Arg Pro Ser Thr Leu Ser Cys Val Asn Thr Pro  
145 150 155 160  
Leu Arg Ser Phe Met Ser Asp Ser Gly Ser Ser Val Asn Gly Val  
165 170 175  
Met Arg Ala Ile Val Lys Ser Pro Ile Met Cys His Glu Lys Ser Pro  
180 185 190  
Ser Val Cys Ser Pro Leu Asn Met Thr Ser Ser Val Cys Ser Pro Ala  
195 200 205  
Gly Ile Asn Ser Val Ser Ser Thr Thr Ala Ser Phe Gly Ser Phe Pro  
210 215 220  
Val His Ser Pro Ile Thr Gln Gly Thr Pro Leu Thr Cys Ser Pro Asn  
225 230 235 240  
Ala Glu Asn Arg Gly Ser Arg Ser His Ser Pro Ala His Ala Ser Asn  
245 250 255  
Val Gly Ser Pro Leu Ser Ser Pro Leu Ser Ser Met Lys Ser Ser Ile  
260 265 270  
Ser Ser Pro Pro Ser His Cys Ser Val Lys Ser Pro Val Ser Ser Pro  
275 280 285  
Asn Asn Val Thr Leu Arg Ser Ser Val Ser Ser Pro Ala Asn Ile Asn  
290 295 300

Asn Ser Arg Cys Ser Val Ser Ser Pro Ser Asn Thr Asn Asn Arg Ser  
 305 310 315 320  
 Thr Leu Ser Ser Pro Ala Ala Ser Thr Val Gly Ser Ile Cys Ser Pro  
 325 330 335  
 Val Asn Asn Ala Phe Ser Tyr Thr Ala Ser Gly Thr Ser Ala Gly Ser  
 340 345 350  
 Ser Thr Leu Arg Asp Val Val Pro Ser Pro Asp Thr Gln Glu Lys Gly  
 355 360 365  
 Ala Gln Glu Val Pro Phe Pro Lys Thr Glu Glu Val Glu Ser Ala Ile  
 370 375 380  
 Ser Asn Gly Val Thr Gly Gln Leu Asn Ile Val Gln Tyr Ile Lys Pro  
 385 390 395 400  
 Glu Pro Asp Gly Ala Phe Ser Ser Cys Leu Gly Gly Asn Ser Lys  
 405 410 415  
 Ile Asn Ser Asp Ser Ser Phe Ser Val Pro Ile Lys Gln Glu Ser Thr  
 420 425 430  
 Lys His Ser Cys Ser Gly Thr Ser Phe Lys Gly Asn Pro Thr Val Asn  
 435 440 445  
 Pro Phe Pro Phe Met Asp Gly Ser Tyr Phe Ser Phe Met Asp Asp Lys  
 450 455 460  
 Asp Tyr Tyr Ser Leu Ser Gly Ile Leu Gly Pro Pro Val Pro Gly Phe  
 465 470 475 480  
 Asp Gly Asn Cys Glu Gly Ser Gly Phe Pro Val Gly Ile Lys Gln Glu  
 485 490 495  
 Pro Asp Asp Gly Ser Tyr Tyr Pro Glu Ala Ser Ile Pro Ser Ser Ala  
 500 505 510  
 Ile Val Gly Val Asn Ser Gly Gln Ser Phe His Tyr Arg Ile Gly  
 515 520 525  
 Ala Gln Gly Thr Ile Ser Leu Ser Arg Ser Ala Arg Asp Gln Ser Phe  
 530 535 540  
 Gln His Leu Ser Ser Phe Pro Pro Val Asn Thr Leu Val Glu Ser Trp  
 545 550 555 560  
 Lys Ser His Gly Asp Leu Ser Ser Arg Arg Ser Asp Gly Tyr Pro Val  
 565 570 575  
 Leu Glu Tyr Ile Pro Glu Asn Val Ser Ser Ser Thr Leu Arg Ser Val  
 580 585 590  
 Ser Thr Gly Ser Ser Arg Pro Ser Lys Ile Cys Leu Val Cys Gly Asp  
 595 600 605  
 Glu Ala Ser Gly Cys His Tyr Gly Val Val Thr Cys Gly Ser Cys Lys  
 610 615 620

Val Phe Phe Lys Arg Ala Val Glu Gly Gln His Asn Tyr Leu Cys Ala  
 625 630 635 640  
 Gly Arg Asn Asp Cys Ile Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro  
 645 650 655  
 Ala Cys Arg Leu Gln Lys Cys Leu Gln Ala Gly Met Asn Leu Gly Ala  
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 Arg Lys Ser Lys Lys Leu Gly Lys Leu Lys Gly Ile His Glu Glu Gln  
 675 680 685  
 Pro Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Ser Pro  
 690 695 700  
 Glu Glu Gly Thr Thr Tyr Ile Ala Pro Ala Lys Glu Pro Ser Val Asn  
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 Thr Ala Leu Val Pro Gln Leu Ser Thr Ile Ser Arg Ala Leu Thr Pro  
 725 730 735  
 Ser Pro Val Met Val Leu Glu Asn Ile Glu Pro Glu Ile Val Tyr Ala  
 740 745 750  
 Gly Tyr Asp Ser Ser Lys Pro Asp Thr Ala Glu Asn Leu Leu Ser Thr  
 755 760 765  
 Leu Asn Arg Leu Ala Gly Lys Gln Met Ile Gln Val Val Lys Trp Ala  
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 Lys Val Leu Pro Gly Phe Lys Asn Leu Pro Leu Glu Asp Gln Ile Thr  
 785 790 795 800  
 Leu Ile Gln Tyr Ser Trp Met Cys Leu Ser Ser Phe Ala Leu Ser Trp  
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 Arg Ser Tyr Lys His Thr Asn Ser Gln Phe Leu Tyr Phe Ala Pro Asp  
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 Leu Val Phe Asn Glu Glu Lys Met His Gln Ser Ala Met Tyr Glu Leu  
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 Cys Gln Gly Met His Gln Ile Ser Leu Gln Phe Val Arg Leu Gln Leu  
 850 855 860  
 Thr Phe Glu Glu Tyr Thr Ile Met Lys Val Leu Leu Leu Ser Thr  
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 Ile Pro Lys Asp Gly Leu Lys Ser Gln Ala Ala Phe Glu Glu Met Arg  
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 Thr Asn Tyr Ile Lys Glu Leu Arg Lys Met Val Thr Lys Cys Pro Asn  
 900 905 910  
 Asn Ser Gly Gln Ser Trp Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu  
 915 920 925  
 Asp Ser Met His Asp Leu Val Ser Asp Leu Leu Glu Phe Cys Phe Tyr  
 930 935 940

Thr Phe Arg Glu Ser His Ala Leu Lys Val Glu Phe Pro Ala Met Leu  
945 950 955 960

Val Glu Ile Ile Ser Asp Gln Leu Pro Lys Val Glu Ser Gly Asn Ala  
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Lys Pro Leu Tyr Phe His Arg Lys  
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<210> 37

<211> 782

<212> DNA

<213> Homo sapiens

<400> 37

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ctgatcttga attcctggcc tgaagtaatc tgcctgcctc agcctccaa agtgctggg 180  
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tgcagagctt cattattttc tttcttc tagt caatcagtcc aaagcacaat gtcagaaaga 720  
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<211> 995

<212> DNA

<213> Homo sapiens

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17 (TNFRSF17)

<400> 38

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gttcttctaa tactcctcctt ctaacatgtc agcgttatttga taatgcaagt gtgaccaatt 360  
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 17 (TNFRSF17)

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				20					25					30			
Pro Pro Leu Thr Cys Gln Arg Tyr Cys Asn Ala Ser Val Thr Asn Ser																	
				35					40					45			
Val Lys Gly Thr Asn Ala Ile Leu Trp Thr Cys Leu Gly Leu Ser Leu																	
				50					55					60			
Ile Ile Ser Leu Ala Val Phe Val Leu Met Phe Leu Leu Arg Lys Ile																	
				65					70					75			80
Ser Ser Glu Pro Leu Lys Asp Glu Phe Lys Asn Thr Gly Ser Gly Leu																	
				85					90					95			
Leu Gly Met Ala Asn Ile Asp Leu Glu Lys Ser Arg Thr Gly Asp Glu																	
				100					105					110			
Ile Ile Leu Pro Arg Gly Leu Glu Tyr Thr Val Glu Glu Cys Thr Cys																	
				115					120					125			
Glu Asp Cys Ile Lys Ser Lys Pro Lys Val Asp Ser Asp His Cys Phe																	
				130					135					140			
Pro Leu Pro Ala Met Glu Glu Gly Ala Thr Ile Leu Val Thr Thr Lys																	
				145					150					155			160
Thr Asn Asp Tyr Cys Lys Ser Leu Pro Ala Ala Leu Ser Ala Thr Glu																	
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Ile Glu Lys Ser Ile Ser Ala Arg																	
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 ggcttagggca gcggcccgaa cccgcacggc tttcttgaa agcgctgccc ctcgcccgg 180  
 cgatgacctc gctgtggaga gaaatcctt tggagtcgt gctggatgt gtttcttgt 240  
 ctctctacca tgacctggaa ccgatgatct attacttcc tttgcaaaca ctagaactca 300

ctggggcttga aggttttagt atagcatttc tttctccaat attcctaaca attatccctt 360  
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gcataggctc ctteccaggct ccaaattgca aacttcgact gatggttctt gcgctgggg 480  
tgtcttcctc actgatagtg caagctgtga cttgggtgtc aggaagtcat ttgcaagg 540  
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agaagactgg tgggttagcc acggggatgg cctctagacc caactggctg ctggcagggg 780  
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cagtaactgct gtgcgtggca agtggattga tgcttccatc ttgttgtgg ttgcgtggta 960  
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acaatgaagg gtggtctagt ctagaaagat cagctcacct gctcaatgaa acaggtgcag 1560  
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ccatgtggct agggaaaag ttgggttct atacagactt tggcataagc acaaggtatc 1680  
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gatatatcac ttccggccat ggctccagag attatctaca gctcaactgaa catggcaatg 1980  
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tggcaaaatt taggatccct gatgacccca ctaattatag agacaaccag aaagtggtca 2160  
tagaccacag agaagtttct gagaattc attttaatcc cagatttggta tcctacaaag 2220  
aaggacacaa ttatgaaaac aaccataatt ttcatatgaa tactcccaa tactttttat 2280  
gaaacattt aacaaagaag ttattggctg gggaaatcta agaaaaaaag tatgtaaatg 2340  
aaaaagaaga gattaatgaa agtggggaaa tacacatgaa gaacctcaac taaaacaca 2400  
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Pro Leu Gln Thr Leu Glu Leu Thr Gly Leu Glu Gly Phe Ser Ile Ala  
35 40 45

Phe Leu Ser Pro Ile Phe Leu Thr Ile Thr Pro Phe Trp Lys Leu Val  
50 55 60

Asn	Lys	Lys	Trp	Met	Leu	Thr	Leu	Leu	Arg	Ile	Ile	Thr	Ile	Gly	Ser
65					70				75				80		
Ile	Ala	Ser	Phe	Gln	Ala	Pro	Asn	Ala	Lys	Leu	Arg	Leu	Met	Val	Leu
			85						90				95		
Ala	Leu	Gly	Val	Ser	Ser	Ser	Leu	Ile	Val	Gln	Ala	Val	Thr	Trp	Trp
				100				105				110			
Ser	Gly	Ser	His	Leu	Gln	Arg	Tyr	Leu	Arg	Ile	Trp	Gly	Phe	Ile	Leu
				115				120				125			o
Gly	Gln	Ile	Val	Leu	Val	Val	Leu	Arg	Ile	Trp	Tyr	Thr	Ser	Leu	Asn
				130				135				140			
Pro	Ile	Trp	Ser	Tyr	Gln	Met	Ser	Asn	Lys	Val	Ile	Leu	Thr	Leu	Ser
145					150					155				160	
Ala	Ile	Ala	Thr	Leu	Asp	Arg	Ile	Gly	Thr	Asp	Gly	Asp	Cys	Ser	Lys
				165					170				175		
Pro	Glu	Glu	Lys	Lys	Thr	Gly	Glu	Val	Ala	Thr	Gly	Met	Ala	Ser	Arg
				180				185				190			
Pro	Asn	Trp	Leu	Leu	Ala	Gly	Ala	Ala	Phe	Gly	Ser	Leu	Val	Phe	Leu
				195				200				205			
Thr	His	Trp	Val	Phe	Gly	Glu	Val	Ser	Leu	Val	Ser	Arg	Trp	Ala	Val
				210				215				220			
Ser	Gly	His	Pro	His	Pro	Gly	Pro	Asp	Pro	Asn	Pro	Phe	Gly	Gly	Ala
225					230				235				240		
Val	Leu	Leu	Cys	Leu	Ala	Ser	Gly	Leu	Met	Leu	Pro	Ser	Cys	Leu	Trp
				245				250				255			
Phe	Arg	Gly	Thr	Gly	Leu	Ile	Trp	Trp	Val	Thr	Gly	Thr	Ala	Ser	Ala
				260				265				270			
Ala	Gly	Leu	Leu	Tyr	Leu	His	Thr	Trp	Ala	Ala	Ala	Val	Ser	Gly	Cys
				275				280				285			
Val	Phe	Ala	Ile	Phe	Thr	Ala	Ser	Met	Trp	Pro	Gln	Thr	Leu	Gly	His
				290				295				300			
Leu	Ile	Asn	Ser	Gly	Thr	Asn	Pro	Gly	Lys	Thr	Met	Thr	Ile	Ala	Met
				305				310				315			320
Ile	Phe	Tyr	Leu	Leu	Glu	Ile	Phe	Phe	Cys	Ala	Trp	Cys	Thr	Ala	Phe
					325				330				335		
Lys	Phe	Val	Pro	Gly	Gly	Val	Tyr	Ala	Arg	Glu	Arg	Ser	Asp	Val	Leu
					340				345				350		
Leu	Gly	Thr	Met	Met	Leu	Ile	Ile	Gly	Leu	Asn	Met	Leu	Phe	Gly	Pro
				355				360				365			
Lys	Lys	Asn	Leu	Asp	Leu	Leu	Leu	Gln	Thr	Lys	Asn	Ser	Ser	Lys	Val
				370				375				380			

Leu Phe Arg Lys Ser Glu Lys Tyr Met Lys Leu Phe Leu Trp Leu Leu  
 385 390 395 400

Val Gly Val Gly Leu Leu Gly Leu Arg His Lys Ala Tyr Glu  
 405 410 415

Arg Lys Leu Gly Lys Val Ala Pro Thr Lys Glu Val Ser Ala Ala Ile  
 420 425 430

Trp Pro Phe Arg Phe Gly Tyr Asp Asn Glu Gly Trp Ser Ser Leu Glu  
 435 440 445

Arg Ser Ala His Leu Leu Asn Glu Thr Gly Ala Asp Phe Ile Thr Ile  
 450 455 460

Leu Glu Ser Asp Ala Ser Lys Pro Tyr Met Gly Asn Asn Asp Leu Thr  
 465 470 475 480

Met Trp Leu Gly Glu Lys Leu Gly Phe Tyr Thr Asp Phe Gly Pro Ser  
 485 490 495

Thr Arg Tyr His Thr Trp Gly Ile Met Ala Leu Ser Arg Tyr Pro Ile  
 500 505 510

Val Lys Ser Glu His His Leu Leu Pro Ser Pro Glu Gly Glu Ile Ala  
 515 520 525

Pro Ala Ile Thr Leu Thr Val Asn Ile Ser Gly Lys Leu Val Asp Phe  
 530 535 540

Val Val Thr His Phe Gly Asn His Glu Asp Asp Leu Asp Arg Lys Leu  
 545 550 555 560

Gln Ala Ile Ala Val Ser Lys Leu Leu Lys Ser Ser Ser Asn Gln Val  
 565 570 575

Ile Phe Leu Gly Tyr Ile Thr Ser Ala Pro Gly Ser Arg Asp Tyr Leu  
 580 585 590

Gln Leu Thr Glu His Gly Asn Val Lys Asp Ile Asp Ser Thr Asp His  
 595 600 605

Asp Arg Trp Cys Glu Tyr Ile Met Tyr Arg Gly Leu Ile Arg Leu Gly  
 610 615 620

Tyr Ala Arg Ile Ser His Ala Glu Leu Ser Asp Ser Glu Ile Gln Met  
 625 630 635 640

Ala Lys Phe Arg Ile Pro Asp Asp Pro Thr Asn Tyr Arg Asp Asn Gln  
 645 650 655

Lys Val Val Ile Asp His Arg Glu Val Ser Glu Lys Ile His Phe Asn  
 660 665 670

Pro Arg Phe Gly Ser Tyr Lys Glu Gly His Asn Tyr Glu Asn Asn His  
 675 680 685

Asn Phe His Met Asn Thr Pro Lys Tyr Phe Leu  
 690 695





### TABLE 25:

**Table 25** depicts SEQ ID NO:, UnigeneID, UnigeneTitle, Pkey, and ExAccn for all of the sequences in Table 26. SEQ ID NO: links the nucleic acid and protein sequence information in Table 26 to Table 25.

Pkey	ExAccn	UnigeneID	Unigene Title	SEQ ID NO:
426101	AL049987		Homo sapiens mRNA; cDNA DKFZp564F112 (fr	1-5
419145	N99638		gb	6 & 7
426818	AA554827	Hs.340046	DKFZp434A0131 protein	8 & 9
421057	T58283		Homo sapiens cDNA	10
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	11 & 12
431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	13 & 14
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	15 & 16
443162	T49951	Hs.9029	DKFZP434G032 protein	17 & 18
436385	BE551618	Hs.144097	ESTs	19-21
447033	AI357412	Hs.157601	ESTs	22 & 23
439608	AW864696	Hs.301732	hypothetical protein MGC5306	24-28
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	29 & 30
442577	AA292998	Hs.163900	ESTs	31 & 32
429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	33 & 34
424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	35 & 36
457407	AA505035	Hs.345911	ESTs	37
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfami	38 & 39
417332	AW972717	Hs.288462	hypothetical protein FLJ21511	40 & 41

**Table 26**

SEQ ID NO:1 DNA sequence

Nucleic Acid Accession #: :

see Table 25 & 25A for complete list

1	11	21	31	41	51	
CAATATAGTA	CAATAACTAT	TTGCATGACA	TTTACATCGG	ATATTATGAG	TGATCTAGAG	60
TTGATATGAA	GTATATGGGA	GGATGTGCAA	AGGTGATGTG	CAAATACTAT	GTCATTTAT	120
AGGGGGGACT	TGAGTATCCT	TTGTTACCT	CAGGAGATCC	TGAAACCAGT	CCCCCATGGA	180
TACTGAGGGC	TGACTGTATA	GTCCTATCCT	CACCGAACCTT	TCATTCTAAT	GGGGGAAGAC	240
TGACTATAAA	CAAAATATAT	GTAATAGGTG	GTGGTAAGTA	CCGTGGAGAA	GTAACAAATG	300
GGGCAAAGTG	AGTTTATACAG	CTCCATTCTT	AGAAACCTTG	GAGTACTTTT	CTTAGTTTAT	360
ACTCGTGGTG	GTTCCTTTT	GTCTCCTTA	TTACATGGGA	CTCTGACATG	TGCCCATAGC	420
TAGGGTGACA	GTAGGATCTA	CCCGATAGTA	GGGTGGCAGT	AGGATCTACC	CAAAAAGCGT	480
CCTGCTGATA	CAGGACAAA	GCATCCTGTT	TTCTCGAGC	CTATAAAAAG	AGCTAATGGT	540
GTTGCTTCTC	TTAACTGTGG	CCTCCTACAC	TGTGTTTGG	ATGATTGGT	ATGTCTTGG	600
TATTCTGTTT	CTTTGGAAC	TTGAATATAC	AACACTTTAC	TAGGGAATTA	GCAATGGAAG	660
CAGAGCAAAG	ATGTACAGAG	GAAACAAATGC	GTAACTCTGA	TGGAATTGAA	GTCATGAGGC	720
AGCAGAGAGC	TTAAATTACA	GCTTTAAAAA	TTTTTATTTT	TTAGAGGGAA	TTTACTTGGG	780
AGTAACAGCA	GTAATAGTTA	ACGGAGCCAG	AATGCTTGAG	TCATATAATT	GCAAAGCAGA	840
GTTGGGAGCA	ACAGATGCTA	AAGAGTAGTT	GCTGTAGTTC	CTCTTGGGT	CGTAGGAGCA	900
GTTGTATAT	TACTATATAG	CTACTGCATG	AAGAAGAGTT	CTTAGTGGAG	CCTGGGTGAA	960
CAGCTCTCT	TAGTATTCTG	TGTGACCCC	TTTGACCTTT	TAACAAATCC	CTAAGTAAAT	1020
AAATAGCCCC	TCAGGAAAAC	TAAGTTTTC	TCTGCTGTTT	TTTTGCTTGA	GAGAGCTATA	1080
ACTGTAATAG	ACTTATATT	CTGAACATT	TAGTGCTTGC	CAATATTG	TAATATTAT	1140
GTTTCCATA	TTTGTATGA	ACATTCTCT	TCCGGTACAT	TTTTTGTAA	ATTATTGTT	1200
GATGGATAAA	AGTTCACCTT	TTATTGTATA	AAATTGACTG	AGATTAATT	ATACACATTG	1260
ACAATGGGT	AATAGAATT	TTCAGATT	AAAAGCTGA	AGGATGACCA	CGTAAGCAAA	1320
AAAAAAAAAA	AAAAAACAA	CAAAAATAA	CCCAAACCCC	TCAAACATT	TCGAACACGA	1380
ACACATTCTC	TGATGCCGGC	ATCCCTGTT	GCAGGTGTGA	AGGGGCAGG	AATCAGCGAG	1440
GTGTCCCTGGG	CTGAGTCCCC	GGGGAAAGAAT	ATGAT			

SEQ ID NO:2 DNA sequence

Nucleic Acid Accession #: X83301.1

1	11	21	31	41	51	
GCAAAGCCAG	CTGGGCTCCT	GAGTCCGGTG	GGTACTTGGA	GAACTTACTA	CGTCTAGCTG	60
GAGGATTGTA	AATGCACCAA	TCAGCATGCT	GTGTCTAGCT	CAAGATTTTC	TCCATCCCC	120
TATTTTGGGC	CAGTGGCTGT	CATTACATAT	GAGATGAGTC	TCTTGAAGAC	TACAGATGAA	180
CTCAAGCTCC	ATGAGGAGAT	GTTCATTGTT	CGAGAGCAGT	CATGATGGCC	TGCACTCCAC	240
ACAATGCAAC	AGAGTGAAAG	AGCAGGTTCT	GCTCTTTGG	TGTAGTCCCTG	AAGCTTCTA	300
AGAAAACCTCA	CATCAGGTGA	TGGATAGGAG	CAACCCGT	AAACCAGCCT	TAGACTATT	360
TTCAAACAGG	CTGGTGAATT	ACCAGATCTC	CGTCAAGTGC	AGTAACCAGT	TCAAGTTGG	420
AGTGTGTCTT	TTGAATGCAG	AGAACAAAGT	CGTGGACAAAC	CAGGCTGGGA	CCCAGGGCCA	480
GCTGAAGGTG	CTGGGTGCCA	ACCTCTGGTG	GCCGTACCTG	ATGCACGAAC	ACCCCGCCTA	540
CCTGTACTCC	TGGGAGGATG	GTGATTGCTC	ACACCAAAGC	CTTGGACCCC	TCCCAGCCTG	600
TGACCTTTGG	GACCAACTCC	ACCTACGCG	CAGACAAGGG	GGCTCTGTAT	GTGGATGTGA	660
TCCGTGTGAA	CAGCTACTAC	TCTTGGTATC	GCAACTACGG	GCACCTGGAG	TTGATTGCG	720
TGCAGCTGGC	CGCCCGATTT	GAGAATTGGT	GTGAGACATC	ACAATCCAT	TATTCAAGAGC	780
GCGTATGGAG	TGGAAACGCT	TGTAGGGTTT	CACCAAGGGCT	GGTGAATTAC	CAGATCTCCG	840
TCAAGTGCAG	TAACCACTTC	AAGTTGGAAG	TATGTCTTTT	GAATGCAGAA	AACAAAGTCG	900
TGGACAACCA	GGCTGGGACC	CAGGGCCAGC	TGAAGGTGCT	GGTGCCAAC	TCTGGTGGCC	960
GTACCTGATG	CACGAACACC	CCGCCTACCT	GTACTCGTGG	GAGGATGGTG	ATTGCTCACA	1020
CCAAAGCCTT	GGACCCCTCC	CAGCCTGTGA	CCTTGGGAC	CAACTCCACC	TACGCAGCAG	1080
ACAAGGGGGC	TCTGTATGTG	GATGTGATCC	GTGTGAACAG	CTACTACTCT	TGGTATCGCA	1140
ACTACGGGCA	CCTGGAGTTG	ATTGGCTGC	AGCCCTGCA	GCTGGCGCC	CAGTTGTGA	1200
ATTGGGTGAA	GACATCACAA	TCCCATTATT	CAGAGCGCGT	ATGGAGTGG	AACGCTTGT	1260

GGGTTTCACC	AGTCTTCCCC	AGGGAACTCC	GATGAAGTGT	TCCAACAAAA	TGAGCGAGTG	1320
AACCAAGAAG	AGGATGACAT	TAGATCCAGG	AGATACAACA	GAGGAGATAA	TCTCCAGGAT	1380
GCCTGTGAAG	AAAGATCCCT	GGATCCCAGG	ATGATTATAG	GACAAGTTGT	TCATAATCCA	1440
GCAGGCCAGA	AGACTTCCAG	GGAAACTCAT	TTCAAGATGA	AAATGGACCA	GCCGCAGTGG	1500
CTCACGCCCT	TAATACCAGC	ACTTTGGGAG	GCTGAGGCAG	GCGGATCACT	TGAGGTCAAG	1560
AGTTTGAAAC	TAGCCTGGCC	AACGTGGCAA	AACTCCATCT	CTATTAAAGA	TACAAAAATT	1620
AGCCAGGCAT	AGTGGTGCAT	GCCTGTAGTC	CCAGCTACTT	GGGATGCTGA	GGCAGGAAGA	1680
ATTGCTTGAA	CCTGGGAGGC	AGAGTCTGCG	GTGACCGAGA	TCATGCCACT	GCACTCCAGC	1740
CTGGGTGACA	GAGCCAGACT	CCGTCTCTAC	AAAAAAAAAA	AAAAAAAAAA	AAA	

SEQ ID NO:3 Protein sequence:  
Protein Accession #: CAA58280.1

1	11	21	31	41	51	
MDRSNPVKPA	LDYFSNRLVN	YQISVKCSNQ	FKLEVCLLNA	ENKVVDNQAG	TQGQLKVLGA	60
NLWWPYLMHE	HPAYLYSWED	GDCSHQSLGP	LPACDLWDQL	HLRSRQGGSV	CGCDPCEQLL	120
LLVSQLRAPG	VDSAAAGRPV					

SEQ ID NO:4 DNA sequence  
Nucleic Acid Accession #: BC002622.1

1	11	21	31	41	51	
GGCACGAGGC	TCCGCCCCGCG	GCCGGGATGC	ACTAGGAAA	GCCAGCTGGG	CTCCTGAGTC	60
CGGTGGGTAC	TTGGAGAACT	TACTACGTCT	AGCTGGAGGA	TTGTAAATGC	ACCAATCAGC	120
ATGCTGTGTC	TAGCTCAAGA	TTTTCTCCAT	CCCTTATTT	TGGGCCAGTG	GCTGTCATTA	180
CATATGAGAA	CTCAAGCTCC	ATGAGGAGAT	GTTTCATTGT	CGAGAGCAGT	CATGATGGCC	240
TGCACTCCAC	ACAATGCAAC	AGAGTAAAG	AGCAGGTTCT	GCTTCTTGG	TGTAGTCCTG	300
AAGCTTCTTA	AGAAACTTCA	CATCAGGTGA	TGGATAGGAG	CAACCCGTGA	AAACCAGCCT	360
TAGACTATT	TTCAAACAGG	CTGGTGAATT	ACCAAGATCTC	CGTCAAGTGC	AGTAACCAGT	420
TCAAGTTGGA	AGTGTGTCTT	TTGAATGCAG	AAAACAAAGT	CGTGGACAAC	CAGGCTGGGA	480
CCCAGGGCCA	GCTGAAGGTG	CTGGGTGCCA	ACCTCTGGTG	GCCGTACCTG	ATGCACGAAC	540
ACCCCGCCTA	CCTGTACTCG	TGGGAGGATG	GTGATTGCTC	ACACCAAAGC	CTTGGACCCC	600
TCCCAGCCTG	TGACCTTGT	GACCAACTCC	ACCTACGCAG	CAGACAAGGG	GGCTCTGTAT	660
GTGGATGTGA	TCCGTGTGAA	CAGCTACTAC	TCTGGTATC	GCAACTACGG	GCACCTGGAG	720
TTGATTTCAGC	TGCAGCTGGC	CGCCCGAGTT	GAGAATTGGT	GTAAGACATC	ACAATCCCAT	780
TATTTCAGAGC	GCGTATGGAG	TGGAAACGCT	TGTAGGGTT	CACCAAGTCTT	TCCCAGGGAA	840
CTCCGATGAA	GTGTCCAAC	AAAATGAGCG	AGTGAACCAA	GAAGAGGATG	ACATTAGATC	900
CAGGAGATAC	AACAGAGGAG	ATAATCTCCA	GGATGCCCTGT	GAAGAAAGAT	CCCTGGATCC	960
CAGGATGATT	ATAGGACAAG	TTGTTCATAA	TCCAGCAGGC	CAGAAGACTT	CCAGGGAAAC	1020
TCATTCAAGG	AGGTAAAAT	GATGGATGAC	TCCTCCAAGA	TGAAATGGA	CCAGCCGCAG	1080
TGGCTCACGC	CTGTAATACC	AGCACTTGG	GAGGCTGAGG	CAGGCGGATC	ACTTGAGGTC	1140
AGGAGTTGA	AACTAGCCTG	GCCAACGTGG	CAAAACTCCA	TCTCTATTAA	AAATACAAAA	1200
ATTAGCCAAG	CATAGTGGTG	CATGCCTGTA	GTCCCAGCTA	CTTGGGATGC	TGAGGCAGGA	1260
AGAATTGCTT	GAACCTGGGA	GGCAGAGTCT	ACAGTGAGCC	GAGATCATGC	CACTGCAC	1320
CAGCCTGGGC	AACACAGTGA	GAATCCATCT	AAAAAAAAAA	AAAAAAAAAA	AA	

SEQ ID NO:5 Protein sequence:  
Protein Accession #: AAH02622.1

1	11	21	31	41	51	
MDRSNPVKPA	LDYFSNRLVN	YQISVKCSNQ	FKLEVCLLNA	ENKVVDNQAG	TQGQLKVLGA	60
NLWWPYLMHE	HPAYLYSWED	GDCSHQSLGP	LPACDLCDSL	HLRSRQGGSV	CGCDPCEQLL	120
LLVSQLRAPG	VDSAAAGRPV					

SEQ ID NO:6 DNA sequence

Nucleic Acid Accession #: :

see Table 25 & 25A for complete list

1	11	21	31	41	51	
ACCTGAGATC	AGGAGTTCGA	GATCAGCCTG	ACCAATAGGG	TGAAACCCCG	TCTCTACTAA	60
AAATAACAAA	AATTAGCTGG	ACACGATGGT	GGGTGCCTGT	GGTCCCCTGCT	ACTCGGGAGG	120
CTGAGACAGG	AGAACATCAGTT	GACCTGGGAG	TTGGTGGTTG	CAGTGAGCTG	AGATCACACC	180
ATTGCATTCC	AAGCCTGGC	AAACAAGAGTG	AAACCTCCATC	GCAAAAAAA	AAAAGAAAGGG	240
GCATAATTG	TGGATGAGGA	TTGGATATAA	GGTAAAGGAT	GGGACATTCT	TGGACTTACA	300
GATGGTGTGA	TTGCCTGGCT	AGAAGAAGAA	TTCCCGGTCA	AAAAGAAACC	ATCAGCTTC	360
CAAGTGTGAA	AGAGAGATAA	ATCTGTGAAG	ATTATAGGGA	CTACAGGAAA	CTTAATCTTT	420
TTCTTGAAA	AAGCAATTGT	AGCAAAAAAA	AAGAAAATT	CTTACTGTCA	TCTAAAATTG	480
ACATGGACAT	CTTAGTGGAC	TAGAAGTAA	GGGCATAAAT	TCTCCCAGTG	ATTTTTAATT	540
TTAGCATTGT	GATTAACACC	TTCTAAAATT	GCCAGAACTT	AATAAAATAAT	TGCTTTTCAT	600
TATTAGTATG	CCATCAAATT	TAGTAGCTGT	TTCAGGCTTT	AATGTGTCAA	GCCTAAAATC	660
CAGATTTTG	AGGATCTTCT	CCCTCTTAAA	AGAGTATTCA	GTAACTGCC	GTAGAAATAC	720
ACATGTATAC	AAGGGCACTG	TATACATCAG	TCTAAAAAAAT	AAAAATATGT	ATACGTTCTG	780
GTGAGTCTAG	CACAGCATTG	CCCAATAGAA	ATACCAATGG	AGGTACACAA	TGTGGCCCAT	840
ATAGGTTAAT	TGGTAAATT	TCTNATAGNC	ACC			

SEQ ID NO:7 DNA sequence

Nucleic Acid Accession #: AK000942

Coding sequence: 1204-1503

1	11	21	31	41	51	
GTAAAGGAAT	GTCTTTTAA	TTCAGCTTT	CTTTTCTCCA	TGCTAGTGTT	ATCAGGTTT	60
GGTATTTATT	TACTTACAGC	ATATGTTATG	AAGCTGGTT	GAAAATTGGT	TTTAGATATA	120
TCTGCAAGTT	TACTACTTTG	ACTGTAAAAA	AAAAAAATGA	AAAAGTAGTT	GACATCTGTC	180
CTCAGAAGAA	GTTTGCAGGT	TGCATATTG	TGTGTAATA	CACAGGCTAA	AAGGTAATT	240
ATGTTCTTG	GGAAATTGAAA	TGGTCAGTGG	CCCCTTACAG	AAACTTATCA	GTCATATATC	300
AGCACCAGTT	CATTCTTTG	CACCTTAGGG	ACCATCTGTC	CCCTGAGGTG	ACCTGAGAAA	360
CAACCAGTTG	CCCACAGACT	GTTATTTCTT	CAAGTGAGCC	AGGATTGAT	TTCACTGCT	420
TATATTCTAT	TTTTAGTGT	CAGTGCTTG	ATTTTTGGAA	AAAACTAAAT	TTAAACATA	480
TTTGAAAAAT	GTTATAAGAC	TTGGACATTA	AGCTGTGTTGA	TAGCCAAAGT	CAGTTTACCA	540
AAGTAAAACA	AATAAATTCT	ATGCTTCTTC	ATTGTCAAAG	AGCAGTCTGC	CATCATGTGG	600
ATATAAATGG	ACTATGTAAA	GTGACATGGT	GCTTACTCTC	TACCTAATAA	TAGCCTCCCT	660
CCTGTTCCAA	CAAGATAACC	AACAGGTATA	TTTAATTAC	CAGTTAATAT	GTTTGGATA	720
ATTGGCTGCC	TTGAAATGCT	ATATGTTTA	TAGTACATCA	TAGCTTTAGT	TTTCTTCATA	780
AGGAAATTAC	AGTTACATCC	TGGCTAACAT	GGTGAAACTC	CATCTCTACT	AAAATACAA	840
AAAATTAGCC	GGGGCGTGGTG	GGGGGCACTT	GTAGTCCCAG	CTACTCGGGA	GGCTGAGGCA	900
GGAGAATGGC	GTGAACCCAG	GAGGCGGAGG	TTGCAGTGAG	CCGAGATCGT	GCCACTGTAC	960
TCTGGCCTGG	GAGACAGAGC	GAGACTCCAT	CTCAAAAAAA	AAAAAAA	AAAAAAAAGA	1020
GAGAGAGAGA	CCTGGAGTAG	AGATTCTGTC	AAAGAACTTT	TTCTTTCTTG	AGAAGCATTCT	1080
GAAATGGAAT	CTGTTGTCTC	TCGAAATAT	GTACTGCTGT	AACAGTGAAA	CAACCCCTCAG	1140
AGTATGCCTT	CGTGTGGGCT	ACTCGTTGT	TTTTGAACT	TGGGGGAAC	GTCTGTGTT	1200
GGGTCAAGAA	TATGCAACTG	GCTGGGCACA	TTGGCTCACG	CCTGTAATCC	CAGCAATTG	1260
GGAGGCTGAG	GCAGGCAGGAT	CACCTGAGGT	CAGGGCTTCA	AGACCAGACT	GGCCAACATG	1320
GTGAAACCCC	GTCTCTACTG	AAAATACAAA	AATTAGCTGG	GCATGGTGGC	AGGTGCCTGT	1380
AATCCCAGCT	ACTCGGGAGG	CTGACGTGAG	AGAATCGCTT	GAACCCGGGA	GTTGGAGGTT	1440
GCAGTGAGCC	GAGATTGCAC	CATTGCACTC	CAGCTGGC	AAACAGAGTG	AAACTCTTGT	1500
CTCAG						

SEQ ID NO:8 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
GACTAGGCTG	GGCAACATAG	TGAGACCTCA	TCTCTAAAAT	TAAAAAAATA	AAAGCCACCA	60
GAAAAAAAACC	AAAAAACATG	CCAAGTGACA	TCAGTCTTTG	ATGAAAATGG	CAGCAGAAGA	120
GTGATGCCAT	GGGTGGGGGT	GGGAAATGCT	ATTTCAGCAG	AGAGGGAGCT	GTCATGGAAG	180
ACACCATGTG	GCTGGGCACG	GTGGCTCACCA	CCTGTAATCC	CAGCACTTTG	GGAGATAGAG	240
GCAGGTGGAT	CCCTTGAGCT	TAGGAATTG	AGACTAGCCT	GGGCAATAAG	AGTGAAACTC	300
CATCTCAAAA	AAAAAAAAAA	AAAAGGTGC	ATGAAACATA	TGAAGCAAAA	AGTGAAAGTC	360
CCCATTCTTT	TCCTTTTCC	AGAGGTGATT	TTTGTGGCCA	ATCTGGTTTC	ATTCCCTCCC	420
AGACACTTTT	CTAGGCATCT	ATGCGCCCT	ATTACACATAT	AAACAAAATA	GGAGTTTCC	480
TGTGCTTCCC	TTAAATGGCA	TATGTATCTT	TCACTCTTTT	TTTCACCTA	GTGGATCTTT	540
AATACCTTAA	AAGCTCAACC	TGGGCTTGGT	GCGGTGGCTC	ATACGTGTAA	TCCCAGGCCT	600
TTGGGAGGCC	AAGTGGGAG	GATCACTTGA	GCTCAGGAGT	TCCAGACCAT	TCCAAAGCAA	660
AAACAAAAGG	ATTTGAGAT	CAGTGTGGC	AACTTAGCAA	AACACCATCT	CTTAAAAAAA	720
AAAAAAAAAA						

SEQ ID NO:9 DNA sequence

Nucleic Acid Accession #: BC010433.1

Coding sequence: 3-335

1	11	21	31	41	51	
GGTCGCCCTC	CGTCGTGGTC	TGGCGTGTAT	TCCGAGCCTT	GGTGTCTGGC	GGTTTCCGAG	60
CGTTGGTGT	TGGCGGTTTC	CGAGCGTTGG	TGTCTGGCGG	TTTCCGACCG	TTGGTGTCTG	120
GCGGTTTCCG	ACCGTTGGTG	TCTGGCACGC	GCCACCCCTCT	CTTGCTTGG	TTGCGCCATG	180
CCGATGTACC	AGACAAGAAG	ACAAGAAAAT	GATTGAGGA	CAGCTTCAT	CGCGGTGTCA	240
AGAAGAAAGC	AGCAAAACGA	CCACTGAAAA	CAACGCCGGT	GGCAAAATAT	CCAAAGAAAG	300
GGTCCAAGC	GGTACATCGT	CATAGCCCGA	AACAGTCAGA	GCCACCAGCC	AATGATCTTT	360
TCAATGCTGC	GAAAGCTGCC	AAAAGTGACA	TGCAACCG	AGAAGTCCGC	GTGAAGTGC	420
TGAAGGCTCT	GAAAGGGCTG	TACGGTAACC	GGGACCTGAC	CGCACGCC	GAGCTCTCA	480
CTGGCCGCTT	CAAGGACTGG	ATGGTTTCCA	TGATCATGGA	CAGAGAGTAC	AGTGTGGCAG	540
TGGAGGCCGT	CAGATTACTG	ATACTTATCC	TTAAGAACAT	GGAAGGGGTG	CTGATGGACG	600
TGGACTGTGA	GAGCGTCTAC	CCCATTGTTG	AGGCCCTCAA	TTGAGGCC	GCCTCTGCTG	660
TGGGTGAATT	TCTGTACTGG	AAACTTTCT	ACCCCTGAGTG	CGAGATAAGA	ACGATGGGTG	720
GAAGAGAGCA	ACGCCAGAGC	CCAGGTGCC	AGAGGACTTT	CTTCCAGCTT	CTGCTGTCT	780
TCTTGTGGA	GAGCAAGCTC	CACGACCACG	CTGCTTACTT	AGTAGACAAC	CTGTGGGACT	840
GTGCAGGGAC	TCAGCTGAAG	GAATGGGAGG	GTCTGACAAG	CCTGCTGCTG	GAGAAGGACC	900
AGAGCACGTG	CCACATGGAG	CCAGGGCCAG	GGACCTTCA	CCTCCTAGGG	TGAAACCAGG	960
AGAGATTGCT	TGCTTCACCT	GTACAAGCA	GGAACGGTGG	CATGGGGTGG	GGGAAACTTG	1020
GAGTTGGAAG	GTGGCTAATC	TTTGATTCTA	TGTTTTGAT	CCTCCTGGCA	CTCCAGACCT	1080
GGGTGATGTG	CAGGAGAGCA	CACTGATAGA	AATCCTTGTG	TCCAGTCCC	AGCAACTCCT	1140
GCCTCAGCCT	CCCGAGCAGC	TGGGACTACA	GGGCCCGCC	ACCACGCC	GCTAACTTTT	1200
TTGTGTTTT	AGTAGAGACG	GGTTTCACC	GTGTTGGCCA	GGATGGTCTT	GATCTCTTG	1260
CCTTGTGATC	CACCTGCCTC	ATCATCCCA	AGTGTGGGA	TTACAGCGT	GAGCCACTGC	1320
GCCCAGCATG	TTAGACAATT	TTAATTCT	CCTCTCTGTG	CTGTTGTTT	CTCAGCTGTG	1380
AAAGGAATAT	TCTGGTGGGG	ACAAGGTTAC	AGAGTTGCTG	AGAGGGCTC	ATGACATGAA	1440
GGTACTGGCC	TTGGCACAGT	GCCTGGGGGG	GCGGGGACTC	CGCACATGCC	TGTGATGTCA	1500
CAGTTACTGT	CAGTCACAG	CGAACCTTCC	CTCCTTTCC	TGTTGACTTT	CCCACACTCC	1560
TGTAACCCTC	CCTCCCTCCC	TTCTCCCTCT	CTCTCTCTCT	CACTCACGCA	CACGCACACA	1620
CACACACACA	CACACACACA	CACACACTCC	ATTCACTGTC	TCCATGACTC	TGGAGTAAAC	1680
TAACGTCTCG	AGTTGCCATT	GGAAGCCCCG	TTGTCCTCAT	TTAGACTTTC	ATGGGTTATA	1740
GGCCTTTTG	ACTTCCCTGGG	GTCCTTCTTC	AGTTAAAAAA	AAAATTAGA	AAATTAGGC	1800
GGCGTGGGT	GCACATGCCT	GTAATCCAG	CACCTTGGCC	TCCCAAAGTG	CTGGGATTAC	1860
AGGAGTGAGC	CACCATGCC	AGCCTCCGTT	GTCCTCATTT	AGACTTTCAT	GGGTTATAGG	1920
CACTTTGAC	TTCCTGGGGT	CCTTCTTCAG	TTAAAAAAA	AAAAAAA	AAAAAAA	

SEQ ID NO:10 DNA sequence

Nucleic Acid Accession #: NM\_000582.1

see Table 25 & 25A for complete list

1	11	21	31	41	51	
AGTGGNTCCC	CCGGNCTGCA	GGAATTGGC	ACGAGATCAT	GATGGCTAAT	ATTCCTGAG	60
CACCTTCAT	TCAGGCATGA	TGCCAGGTGC	ACCAACTTAC	TTAACCTCTA	TAGCCACCAC	120
CTGAGCAAGC	TCCTGTTTTA	TAAATGGACC	AGTTCTTGTT	GCTGTTGTAC	AAGTTATT	180
CTTTCTATAA	CGTCCTCCTT	GTCCTCCTTC	CACATTCTTA	AAGAAACCTT	CCCTTCCTT	240
AAAGTACTCA	GGGAGCCCTG	CATTGCTCT	TGAAGCCTTC	TCCAGCTTCA	TCATCTCAC	300
GTGGTCTCTC	TTTCACTAA	ATGTCCAATA	TGCTGCACAT	AAGTACCCCA	AAGTTAGCAC	360
AGGAATTGTT	CCATGGCTGT	CATATATGTT	AAAATCATT	AAAAGTTCAT	TTTTCTCTC	420
ATTATGGGAA	GGATACATGC	TCCTACTAGT	AAATTTAGTA	GGTAGAAAAA	AATTATCACT	480
ATCTAGACTG	CTTCCATT	AGTCTTATG	CATAGCTTTC	GTGCTGCCT	ATTTTACCT	540
TGTGTTGTA	ACTTACTATT	ATAAAATATG	CGTCTCTATG	TTCATTGTCA	ACGATTATT	600
ACAATAACAT	GGAGTGGATT	TACATGTATT	CTCTATATT	GGATTAAAGG	AGATAGAGTA	660
TGTGAAATT	AATGGGAGAA	GTATCTGATA	CATAACAGGC	AATACAAATA	TTATCACATA	720
GCGTCAATT	ATTTGTGAAT	ATTGAAAGCT	CCAAAAAAGA	AAAAAAGTT	TTTTTTAATT	780
CCCGTAATT	CTTATTGCAG	TATTGTTTC	ATACAAACTG	CTCAGTCATT	TTGGAGAAAT	840
ACAATTTT	TTCCCTCATCA	TGAAGTAAGG	TATGCTCACT	GCAAAAAAAA	TCTAGAAAAT	900
AAAGAGGAAC	ATGCTAAAGA	AAAGAATACT	CCCATAATAAT	CTCTGTCTTC	ATAAATAATC	960
TTTGTAACG	CTTATACACT	GCTGGTGGGA	ATGTAAATT	GTTCAGCCAT	TGTGAAAAGT	1020
ACCGTAGCAA	TTCCCTGAAA	AACTTAAAT	AGATTTACCG	TTCAACCCAG	CAATCCCATT	1080
ATTGGGCATA	TACCCAGTGG	AATGTAATC	ATCCTGCCAT	AAAAACACAT	GCACATGTAT	1140
GTTCATTGCA	GCACATTTC	CAATAGCAAA	GACATGGAAT	CAACCTATAT	GCCCCATCAAT	1200
AGTAGACTGA	ATAAAGAAAA	TATGGTACAT	ATTCAACCACA	GAATACTAAG	CAGCCATAAA	1260
AAAAAA						

SEQ ID NO:11 DNA sequence

Nucleic Acid Accession #: NM\_000582.1

Coding sequence: 88-990

1	11	21	31	41	51	
GCAGAGCACA	GCATCGTCGG	GACCAGACTC	GTCTCAGGCC	AGTTGCAGCC	TTCTCAGCCA	60
AACCCGACCC	AAGGAAAAC	CACTACCATG	AGAATTGCAG	TGATTGCTT	TTGCCTCTA	120
GGCATCACCT	GTGCCATACC	AGTTAACACAG	GCTGATTCTG	GAAGTTCTGA	GGAAAAGCAG	180
CTTTACAACA	AATACCCAGA	TGCTGTGGCC	ACATGGCTAA	ACCCTGACCC	ATCTCAGAAG	240
CAGAATCTCC	TAGCCCCACA	GACCCTTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCACATG	300
GATGATATGG	ATGATGAAGA	TGATGATGAC	CATGTGGACA	GCCAGGACTC	CATTGACTCG	360
AACGACTCTG	ATGATGTAGA	TGACACTGT	GATTCTCACC	AGTCTGATGA	GTCTCACCAT	420
TCTGATGAAT	CTGATGAACT	GGTCACTGT	TTTCCCACGG	ACCTGCCAGC	AACCGAAGTT	480
TTCACTCCAG	TTGTCCCCAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGGTTAT	540
GGACTGAGGT	CAAAATCTAA	GAAGTTTCGC	AGACCTGACA	TCCAGTACCC	TGATGCTACA	600
GACGAGGACA	TCACCTCACA	CATGGAAGC	GAGGAGTTGA	ATGGTCATA	CAAGGCCATC	660
CCCGTTGCC	AGGACCTGAA	CGCGCCTCT	GATTGGGACA	GCCGTGGAA	GGACAGTTAT	720
GAAACGAGTC	AGCTGGATGA	CCAGAGTGT	GAAACCCACA	GCCACAAGCA	GTCCAGATTA	780
TATAAGCGGA	AAGCCAATGA	TGAGAGCAAT	GAGCATTCCG	ATGTGATTGA	TAGTCAGGAA	840
CTTTCACAAAG	TCAGCCGTGA	ATTCCACAGC	CATGAATTTC	ACAGCCATGA	AGATATGCTG	900
GTTGTAGACC	CCAAAAGTAA	GGAGAAGAT	AAACACCTGA	AATTCGTAT	TTCTCATGAA	960
TTAGATAGTG	CATCTCTGA	GGTCATTAA	AAGGAGAAA	AATACAATT	CTCACTTTGC	1020
ATTTAGTCAA	AAGAAAAAAAT	GCTTTATAGC	AAAATGAAAG	AGAACATGAA	ATGCTTCTT	1080
CTCAGTTTAT	TGGTTGAATG	TGTATCTATT	TGAGTCTGGA	AATAACTAAT	GTGTTGATA	1140
ATTAGTTTAG	TTTGTGGCTT	CATGGAAACT	CCCTGTAAAC	AAAAGCTTC	AGGGTTATGT	1200
CTATGTTCAT	TCTATAGAAG	AAATGCAAAC	TATCACTGTA	TTTTAATATT	TGTTATTCTC	1260
TCATGAATAG	AAATTATGT	AGAAGCAAAC	AAAATACTT	TACCCACTTA	AAAAGAGAAT	1320
ATAACATTT	ATGTCACTAT	AATCTTTGT	TTTTAAGTT	AGTGTATATT	TTGTTGTGAT	1380
TATCTTTTG	TGGTGTGAAT	AAATCTTTA	TCTTGAATGT	AATAAGAATT	TGGTGGGTGTC	1440
AATTGCTTAT	TTGTTTCCC	ACGGTTGTCC	AGCAATTAAT	AAAACATAAC	CTTTTTACT	1500
GCCTAAAAAA	AAAAAA	AAAAAA	AAAA			

SEQ ID NO:12 Protein sequence:  
Protein Accession #: NP\_000573.1

1	11	21	31	41	51	
MRIAVICFL	LGITCAIPVK	QADSGSSEEK	QLYNKYPDAV	ATWLNPDPHQ	KQNLLAPQTL	60
PSKSNESHDH	MDMMDEDDEDD	DHVDSQDSID	SNDSDDVDDT	DDSHQSDESH	HSDESDELVT	120
DFPTDLPATE	VFTPVVPTVD	TYDGRGDSVV	YGLRSKSKKF	RRPDIQYPDA	TDEDITSHME	180
SEELNGAYKA	IPVAQDLNAP	SDWDSRGKDS	YETSQLDDQS	AETHSHKQSR	LYKRKANDES	240
NEHSDVIDSQ	ELSKVSREFH	SHEFHSHEDM	LVVDPKSKEE	DKHLKFRISEH	ELDSASSEVN	

SEQ ID NO:13 DNA sequence  
Nucleic Acid Accession #: NM\_001793  
Coding sequence: 71-2560

1	11	21	31	41	51	
AAAGGGGCAA	GAGCTGAGCG	GAACACCGGC	CCGCCGTGCG	GGCAGCTGCT	TCACCCCTCT	60
CTCTGCAGCC	ATGGGGCTCC	CTCGTGGACC	TCTCGCGTCT	CTCCTCCTTC	TCCAGGTTTG	120
CTGGCTGCAG	TGCGCGGCCT	CCGAGCCGTG	CCGGGCGGTC	TTCAGGGAGG	CTGAAGTGAC	180
CTTGGAGGCG	GGAGGCGCGG	AGCAGGAGCC	CGGCCAGGCG	CTGGGGAAAG	TATTCACTGGG	240
CTGCCCTGGG	CAAGAGCCAG	CTCTGTTTAG	CACTGATAAT	GATGACTTCA	CTGTGCGGAA	300
TGGCGAGACA	GTCCAGGAAA	GAAGGTCACT	GAAGGAAAGG	AATCCATTGA	AGATCTTCCC	360
ATCCAAACGT	ATCTTACGAA	GACACAAAGAG	AGATTGGGTG	GTTGCTCCAA	TATCTGTCCC	420
TGAAAATGGC	AAGGGTCCCT	TCCCCCAGAG	ACTGAATCAG	CTCAAGTCTA	ATAAAGATAG	480
AGACACCAAG	ATTTTCTACA	GCATCACGGG	GCCGGGGGCA	GACAGCCCCC	CTGAGGGTGT	540
CTTCGCTGTA	GAGAAGGAGA	CAGGCTGTT	GTTGTTGAAT	AAGCCACTGG	ACCGGGAGGA	600
GATTGCCAAG	TATGAGCTCT	TTGGCCACCG	TGTGTCAGAG	AATGGTGCCT	CAGTGGAGGA	660
CCCCATGAAC	ATCTCCATCA	TCGTGACCGA	CCAGAATGAC	CACAAGCCCA	AGTTTACCCA	720
GGACACCTTC	CGAGGGAGTG	TCTTAGAGGG	AGTCTTACCA	GGTACTTCTG	TGATGCAGGT	780
GACAGCCACG	GATGAGGATG	ATGCCATCTA	CACCTACAAT	GGGGTGGTTG	CTTACTCCAT	840
CCATAGCCAA	GAACCAAAGG	ACCCACACGA	CCTCATGTTC	ACCATTCAACC	GGAGCACAGG	900
CACCATCAGC	GTCATCTCCA	GTGGCCTGGA	CCGGGAAAAAA	GTCCCTGAGT	ACACACTGAC	960
CATCCAGGCC	ACAGACATGG	ATGGGGACGG	CTCCACCACCC	ACGGCAGTGG	CAGTAGTGGA	1020
GATCCTTGAT	GCCAATGACA	ATGCTCCAT	GTTGACCCCC	CAGAAGTACG	AGGCCATGTT	1080
GCCTGAGAACAT	GCAGTGGGCC	ATGAGGTGCA	GAGGCTGACG	GTCACTGATC	TGGACGCC	1140
CAACTCACCA	GCGTGGCGTG	CCACCTACCT	TATCATGGGC	GGTGACGACG	GGGACCATTT	1200
TACCATCACC	ACCCACCCCTG	AGAGCAACCA	GGGCATCCTG	ACAACCAGGA	AGGGTTTGGA	1260
TTTGAGGCC	AAAAACCAAGC	ACACCTGTG	CGTGTGAAGTG	ACCAACGAGG	CCCCTTTGT	1320
GCTGAAGCTC	CCAAACCTCCA	CAGCCACCAT	AGTGGTCCAC	GTGGAGGATG	TGAATGAGGC	1380
ACCTGTGTT	GTCCCACCCCT	CCAAAGTCGT	TGAGGTCCAG	GAGGGCATCC	CCACTGGGGA	1440
GCCTGTGTGT	GTCTACACTG	CAGAAGACCC	TGACAAGGAG	AATCAAAAGA	TCAGCTACCG	1500
CATCCTGAGA	GACCCAGCAG	GGTGGCTAGC	CATGGACCCA	GACAGTGGGC	AGGTCAACAGC	1560
TGTGGCACC	CTCGACCGTG	AGGATGAGCA	GTTTGTGAGG	AACAACATCT	ATGAAGTCAT	1620
GGTCTGGCC	ATGGACAATG	GAAGCCCTCC	CACCACTGGC	ACGGGAACCC	TTCTGCTAAC	1680
ACTGATTGAT	GTCAATGACC	ATGGCCCACT	CCCTGAGCCC	CGTCAGATCA	CCATCTGCAA	1740
CCAAAGCCCT	GTGCCAGCAGG	TGCTGAACAT	CACGGACAAG	GACCTGTCTC	CCCACACCTC	1800
CCCTTCCAG	GCCCAGCTCA	CAGATGACTC	AGACATCTAC	TGGACGGCAG	AGGTCAACGA	1860
GGAAGGTGAC	ACAGTGGCT	TGTCCTGAA	GAAGTTCCCTG	AAGCAGGATA	CATATGACGT	1920
GCACCTTCT	CTGCTGACCC	ATGGCAACAA	AGAGCAGCTG	ACGGTGATCA	GGGCCACTGT	1980
GTGCGACTGC	CATGCCATG	TCGAAACCTG	CCCTGGACCC	TGGAAGGGAG	TTTCATCCT	2040
CCCTGTGCTG	GGGGCTGTCC	TGGCTCTGCT	GTTCCTCCTG	CTGGTGCTGC	TTTTGTTGGT	2100
GAGAAAGAAG	CGGAAGATCA	AGGAGCCCT	CCTACTCCCA	GAAGATGACA	CCCGTGACAA	2160
CGTCTCTAC	TATGGCGAAG	AGGGGGTGG	CGAAGAGGAC	CAGGACTATG	ACATCACCCA	2220
GCTCCACCGA	GGTCTGGAGG	CCAGGCCGGA	GGTGGTTCTC	CGCAATGACG	TGGCACCAAC	2280
CATCATCCCC	ACACCCATGT	ACCGTCCTCG	GCCAGCCAAC	CCAGATGAAA	TCGGCAACTT	2340
TATAATTGAG	AACCTGAAGG	CGGCTAACAC	AGACCCCCACA	GCCCCGCCCT	ACGACACCC	2400
CTTGGTGTTC	GACTATGAGG	GCAGCGGCTC	CGACGCCGCG	TCCCTGAGCT	CCCTCACCTC	2460
CTCCGCCCTCC	GACCAAGACC	AAGATTACGA	TTATCTGAAC	GAGTGGGGCA	GCCGCTTCAA	2520
GAAGCTGGCA	GACATGTACG	GTGGCGGGGA	GGACGACTAG	CGGGCCTGCC	TGCAGGGCTG	2580

GGGACCAAAAC	GTCAGGCCAC	AGAGCATCTC	CAAGGGTCT	CAGTTCCCCC	TTCAGCTGAG	2640
GA CTTCTGGAG	CTTGTCA GAGGA	AGTGGCCGTA	GCAACTTGGC	GGAGACAGGC	TATGAGCTG	2700
ACGTTAGAGT	GGTTGCTTCC	TTAGCCTTTC	AGGATGGAGG	AATGTGGCA	GT TTTGACTTC	2760
AGCACTGAAA	ACCTCTCCAC	CTGGGCCAGG	GTTGCCTCAG	AGGCCAAGTT	TCCAGAAGCC	2820
TCTTACCTGC	CGTAAAATGC	TCAACCCCTGT	GTCCTGGCC	TGGGCCGCT	GTGACTGACC	2880
TACAGTGGAC	TTTCTCTCTG	GAATGGAACC	TTCTTAGGCC	TCCTGGTGCA	ACTTAATT	2940
TTTTTTAAAT	GCTATCTTCA	AAACGTTAGA	GAAAGTTCTT	CAA AAAGTGCA	GCCCAGAGCT	3000
GCTGGGCCCA	CTGGCGTCC	TGCATTCTG	GTTCCAGAC	CCC AATGCCT	CCCATTGGA	3060
TGGATCTCTG	CGTTTTATA	CTGAGTGTGC	CTAGGTTGCC	CCTTATT	TATTTCCCT	3120
GT TTCGTTGC	TATAGATGAA	GGGTGAGGAC	AATCGTGTAT	ATGTACTAGA	ACTTTTTAT	3180
TAAAGAAACT	TTTCCCAGAA	AAAAAA				

SEQ ID NO:14 Protein sequence:  
Protein Accession #: NP\_001784.2

1	11	21	31	41	51	
MGLPRGPLAS	LLLLQVCWLQ	CAASEPCRAV	FREAEVTLEA	GGAEQEPEQQA	LGKVFMGCPG	60
QEPALFSTDN	DDFTVRNGET	VQERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG	120
KGPFPQRNLQ	LKSNKDRDTK	IFYSITGPG	DSPPEGVFAV	EKETGWLLLN	KPLDREEIAK	180
YELFGHAVSE	NGASVEDPMN	ISIIVTDQND	HKPKFTQDTF	RGSVLEGVLP	GTSVMQVTAT	240
DEDDAIYTYN	GVVAYSIIHSQ	EPKDPHDLMF	TIHRSTGTIS	VISSGLDREK	VPEYTLTIQA	300
TDMDGDGSTT	TAVAVVEILD	ANDNAPMFDP	QKYEAHVPE	AVGHEVQRLT	VTLDLAPNSP	360
AWRATYLI	IMG GDDGDHFTIT	THPESNQGIL	TTRKGLDFEA	KNQHTLYVEV	TNEAPFVLKL	420
PTSTATIVWH	VEDVNEAPVF	VPPSKVVEVQ	E GIPTGE	VYTAEDPDKE	NQKISYRILR	480
DPAGWLAMDP	DSGQVTAVGT	LDREDEQFVR	NNIYEVMVLA	MDNGSPPTTG	TGTLLLTLID	540
VNDHGPVPEP	RQITICNQSP	VRQLVNITDK	DLS PHTSPFQ	AQLTDDSDIY	WTAEVNEEGD	600
TVVLSLKKFL	KQDTYDVHLS	LSDHGNKEQL	T VIRATVCDC	HGHVETCPGP	WKGGFILPVL	660
GAVLALLFL	LVLLLVRKK	RKIKEPLLLP	EDDTRDNVFY	YGEEGGGEED	QDYDITQLHR	720
GLEARPEVVL	RNDVAPTIIP	TPMYRPRPAN	PDEIGNFIIE	NLKAANTDPT	APPYDTLLVF	780
DYEGSGSDAA	SLSSLTSSAS	DQDQDYDYL	EWGSRFKKLA	DMYGGGEDD		

SEQ ID NO:15 DNA sequence  
Nucleic Acid Accession #: XM\_051860.2  
Coding sequence: 261-4346

1	11	21	31	41	51	
GAGCTAGCGC	TCAAGCAGAG	CCCAGGCCGG	TGCTTATCGGA	CAGAGCCTGG	CGAGCGCAAG	60
CGCGCGGGGG	AGCCAGCGGG	GCTGAGCGCG	GCCAGGGTCT	GAACCCAGAT	TT CCCAGACT	120
AGCTACCACT	CCGCTTGCCC	ACGCCCCGGG	AGCTCGCGC	GCCTGGCGGT	CAGCGACCAG	180
ACGTCCGGGG	CCGCTGCGCT	CCTGGCCCGC	GAGGC GTGAC	ACTGTCTCGG	CTACAGACCC	240
AGAGGGAGCA	CACTGCCAGG	ATGGGAGCTG	CTGGGAGGCC	GGACTTCTCT	TTCAAGGCCA	300
TGCTGACCAT	CAGCTGGCTC	ACTCTGACCT	GCTTCCCTGG	GGCCACATCC	ACAGTGGCTG	360
CTGGGTGCC	TGACCAGAGC	CCTGAGTTGC	AACCC CTGGGAA	CCCTGGCCAT	GACCAAGACC	420
ACCATGTGCA	TATCGGCCAG	GGCAAGACAC	TGCTGCTCAC	CTCTTCTGCC	ACGGTCTATT	480
CCATCCACAT	CTCAGAGGGA	GGCAAGCTGG	TCATTAAAGA	CCACGACGAG	CCGATTGTT	540
TGCGAACCCG	GCACATCCTG	ATTGACAACG	GAGGAGAGCT	GCATGCTGGG	AGTGC CCCTCT	600
GCCCTTCCA	GGGCAATTTC	ACCATCATT	TGTATGGAAAG	GGCTGATGAA	GGTATT CAGC	660
CGGATCCTTA	CTATGGTCTG	AAGTACATTG	GGGTTGGTAA	AGGAGGC GCT	CTTGAGTTGC	720
ATGGACAGAA	AAAGCTCTCC	TGGACATTTC	TGAACAAGAC	CCTTCACCCA	GGTGG CATGG	780
CAGAAGGAGG	CTATTTTTT	GAAAGGAGCT	GGGGCCACCG	TGGAGTTATT	GTT CATGTCA	840
TCGACCCCAA	ATCAGGCACA	GTCATCCATT	CTGACCGGTT	TGACACCTAT	AGATCCAAGA	900
AAGAGAGTGA	ACGTCTGGTC	CAGTATT TGA	ACGCGGTGCC	CGATGGCAGG	ATC CTTCTCTG	960
TTGCAGTGAA	TGATGAAGGT	TCTCGAA ATC	TGGATGACAT	GGCCAGGAAG	GCGATGACCA	1020
AATTGGGAAG	CAAACACTTC	CTGCACCTT	GATTAGACA	CCCTTGGAGT	TTT CTAACTG	1080
TGAAAGGAAA	TCCATCATCT	TCAGTGGAAAG	ACC ATATTGA	ATATCATGGA	CATCGAGGCT	1140
CTGCTGCTGC	CCGGTATT	AAATTGTTCC	AGACAGAGCA	TGG CGAATAT	TTCAATGTT	1200
CTTTGTCCAG	TGAGTGGGTT	CAAGACGTGG	AGTGGACGGA	GTGG TCGAT	CATGATAAAG	1260

TATCTCAGAC	TAAAGGTGGG	GAGAAAATT	CAGACCTCTG	GAAAGCTCAC	CCAGGAAAAA	1320
TATGCAATCG	TCCCATTGAT	ATACAGGCCA	CTACAATGGA	TGGAGTTAAC	CTCAGCACCG	1380
AGGTTGTCTA	CAAAAAAAGGC	CAGGATTATA	GGTTTGCTTG	CTACGACCGG	GGCAGAGCCT	1440
GCCGGAGCTA	CCGTGTACGG	TTCCCTCTGTG	GGAAAGCCTGT	GAGGCCAAA	CTCACAGTCA	1500
CCATTGACAC	CAATGTGAAC	AGCACCATTC	TGAACCTGGA	GGATAATGTA	CAGTCATGGA	1560
AACCTGGAGA	TACCCCTGGTC	ATTGCCAGTA	CTGATTACTC	CATGTACCAAG	GCAGAAGAGT	1620
TCCAGGGTCT	TCCCCTGCAGA	TCCTGCGCCC	CCAACCAGGT	CAAAGTGGCA	GGGAAACCAA	1680
TGTACCTGCA	CATCGGGGAG	GAGATAGACG	GCGTGGACAT	CGGGCGGGAG	GTGGGGCTTC	1740
TGAGCCGGAA	CATCATAGT	ATGGGGGAGA	TGGAGGACAA	ATGCTACCCC	TACAGAAACC	1800
ACATCTGCAA	TTTCTTGAC	TTCGATACCT	TTGGGGGCCA	CATCAAGTT	GCTCTGGAT	1860
TTAAGGCAGC	ACACTTGGAG	GGCACGGAGC	TGAAGCATAT	GGGACAGCAG	CTGGTGGGTC	1920
AGTACCCGAT	TCACTTCCAC	CTGGCCGGTG	ATGTAGACGA	AAGGGGAGGT	TATGACCCAC	1980
CCACATACAT	CAGGGACCTC	TCCATCCATC	ATACATTCTC	TCGCTGCGTC	ACAGTCCATG	2040
GCTCCAATGG	CTTGGTGTAC	AAGGACGTTG	TGGGCTATAA	CTCTTGGC	CACTGTTCT	2100
TCACGGAAGA	TGGGCCGGAG	GAACGCAACA	CTTTTGACCA	CTGTCTTGGC	CTCCTTGTCA	2160
AGTCTGGAAC	CCTCCTCCCC	TCGGACCGTG	ACAGCAAGAT	GTGCAAGATG	ATCACAGAGG	2220
ACTCCTACCC	GGGGTACATC	CCCAAGCCCA	GGCAAGACTG	CAATGCTGTG	TCCACCTTCT	2280
GGATGGCCAA	TCCCAACAAAC	AACCTCATCA	ACTGTGCCGC	TGCAGGATCT	GAGGAAACTG	2340
GATTTGGTT	TATTTTCAC	CACGTACCAA	CGGGCCCCCTC	CGTGGGAATG	TACTCCCCAG	2400
GTTATTCA	GCACATTCCA	CTGGGAAAAT	TCTATAACAA	CCGAGCACAT	TCCAACCTACC	2460
GGGCTGGCAT	GATCATAGAC	AACGGAGTC	AAACCACCGA	GGCCTCTGCC	AAGGACAAGC	2520
GGCCGTTCC	CTCAATCATC	TCTGCCAGAT	ACAGCCCTCA	CCAGGACGCC	GACCCGCTGA	2580
AGCCCCGGGA	GCCGCCATC	ATCAGACACT	TCATTGCCCTA	CAAGAACCAAG	GACCACGGGG	2640
CCTGGCTGCG	CGGGGGGGAT	GTGTGGCTGG	ACAGCTGCCG	GTGGCTGAC	AATGGCATTG	2700
GCCTGACCC	GGCCAGTGGT	GGAACCTTCC	CGTATGACGA	CGGCTCCAAG	CAAGAGATAA	2760
AGAACAGCTT	GTGGTGTGGC	GAGAGTGGCA	ACGTGGGAC	GGAAATGATG	GACAATAGGA	2820
TCTGGGGCCC	TGGCGGCTTG	GACCATAGCG	GAAGGACCCCT	CCCTATAGGC	CAGAATTTTC	2880
CAATTAGAGG	AATTCACTTA	TATGATGGCC	CCATCAACAT	CCAAACTGC	ACTTTCCGAA	2940
AGTTTGTGGC	CCTGGAGGGC	CGGCACACCA	GCGCCCTGGC	CTTCCGCCCTG	AATAATGCCT	3000
GGCAGAGCTG	CCCCCATAAC	AACGTGACCG	GCATTGCCCT	TGAGGACGTT	CCGATTACTT	3060
CCAGAGTGT	CTTGGGAGAG	CCTGGGCCCT	GGTCAACCA	GCTGGACATG	GATGGGGATA	3120
AGACATCTGT	GTTCCATGAC	GTCGACGGCT	CCGTGTCCGA	GTACCCCTGGC	TCCTACCTCA	3180
CGAAGAATGA	CAACTGGCTG	GTCCGGCAC	CAGACTGCAT	CAATGTTCCC	GACTGGAGAG	3240
GGGCCATTG	CAGTGGGTGC	TATGCACAGA	TGTACATTCA	AGCCTACAAAG	ACCAGTAACC	3300
TGCGAATGAA	GATCATCAAG	AATGACTTCC	CCAGGCCACCC	TCTTTACCTG	GAGGGGGCGC	3360
TCACCAGGAG	ACCCATTAC	CAGCAATACC	AACCGGTTGT	CACCCCTGCAG	AAGGGCTACA	3420
CCATCCACTG	GGACCAAGACG	GCCCCGGCCG	AACTGCCAT	CTGGCTCATC	AACTTCAACA	3480
AGGGCGACTG	GATCCGAGTG	GGGCTCTGCT	ACCCGCGAGG	CACCACTTC	TCCATCCTCT	3540
CGGATGTTCA	CAATCGCTG	CTGAAGCAAA	CGTCCAAGAC	GGGCGTCTTC	GTGAGGACCT	3600
TGCAGATGGA	CAAAGTGGAG	CAGAGCTACC	CTGGCAGGAG	CCACTACTAC	TGGGACGAGG	3660
ACTCAGGGCT	GTTGTTCTG	AAGCTGAAAG	CTCAGAACGA	GAGAGAGAAG	TTTGCTTTCT	3720
GCTCCATGAA	AGGCTGTGAG	AGGATAAAGA	TTAAAGCTCT	GATTCCAAAG	AACGCAGGGC	3780
TCAGTGA	CACAGCCACA	GCTTACCCCA	AGTCACCGA	GAGGGCTGTC	GTAGACGTGC	3840
CGATGCCAA	GAAGCTCTTT	GGTTCTCAGC	TGAAAACAAA	GGACCATTTC	TTGGAGGTGA	3900
AGATGGAGAG	TTCCAAGCAG	CACTCTTCC	ACCTCTGGAA	CGACTTCGCT	TACATTGAAG	3960
TGGATGGAA	GAAGTACCCC	AGTTCGGAGG	ATGGCATCCA	GGTGGTGGTG	ATTGACGGGA	4020
ACCAAGGGCG	CGTGGTGGAC	CACACGAGCT	TCAGGAACCTC	CATTCTGCAA	GGCATAACCAT	4080
GGCAGCTTT	CAACTATGTG	GCGACCATCC	CTGACAATT	CATAGTGCTT	ATGGCATCAA	4140
AGGGAAAGATA	CGTCTCCAGA	GGCCCATGGA	CCAGAGTGCT	GGAAAAGCTT	GGGGCAGACA	4200
GGGGTCTCAA	GTGAAAGAG	CAAATGGCAT	TCGTTGGCTT	CAAAGGCAGC	TTCCGGCCCA	4260
TCTGGGTGAC	ACTGGACACT	GAGGATCACA	AAGCCAAAAT	CTTCCAAGTT	GTGCCCATCC	4320
CTGTGGTGA	GAAGAAGAAG	TTGTGAGGAC	AGCTGCCGCC	CGGTGCCACC	TCGTGGTAGA	4380
CTATGACGGT	GACTCTTGGC	AGCAGACCA	TGGGGATGG	CTGGGCTCCC	CAGCCCTG	4440
CAGCAGCTGC	CTGGGAAGGC	CGTGTTCAG	CCCTGATGGG	CCAAGGGAAG	GCTATCAGAG	4500
ACCCTGGTGC	TGCCACCTGC	CCCTACTCAA	GTGTCTACCT	GGAGCCCTG	GGCGGGTGCT	4560
GGCCAATGCT	GGAAACATT	ACTTTCTGC	AGCCTCTTGG	GTGCTTCTCT	CCTATCTGTG	4620
CCTCTTCAGT	GGGGTTTGG	GGACCATATC	AGGAGACCTG	GGTTGTGCTG	ACAGCAAAGA	4680
TCCACTTTGG	CAGGAGCCCT	GACCCAGCTA	GGAGGTAGTC	TGGAGGGCTG	GTCATTCA	4740
GATCCCCATG	GTCTTCAGCA	GACAAGTGGAG	GGTGGTAAAT	GTAGGAGAAA	GAGCCTTGGC	4800
CTTAAGGAAA	TCTTACTCC	TGTAAGCAAG	AGCCAACCTC	ACAGGATTAG	GAGCTGGGTT	4860
AGAACTGGCT	ATCCTTGGGG	AAGAGGCAAG	CCCTGCCCTCT	GGCGTGTCC	ACCTTCAGG	4920

AGACTTTGAG	TGGCAGGTTT	GGACTTGGAC	TAGATGACTC	TCAAAGGCC	TTTTAGTTCT	4980
GAGATTCCAG	AAATCTGCTG	CATTTCACAT	GGTACCTGGA	ACCCAACAGT	TCATGGATAT	5040
CCACTGATAT	CCATGATGCT	GGGTGCCCA	GCGCACACGG	GATGGAGAGG	TGAGAACTAA	5100
TGCCTAGCTT	GAGGGGTCTG	CAGTCCAGTA	GGGCAGGCAG	TCAGGTCCAT	GTGCACTGCA	5160
ATGCCAGGTG	GAGAAATCAC	AGAGAGGTAA	AATGGAGGCC	AGTGCCATT	CAGAGGGGAG	5220
GCTCAGGAAG	GCTTCTTGCT	TACAGGAATG	AAGGCTGGGG	GCATTTGCT	GGGGGGAGAT	5280
GAGGCAGCCT	CTGGAATGGC	TCAGGGATT	AGCCCTCCCT	GCCGCTGCCT	GCTGAAGCTG	5340
GTGACTACGG	GGTCGCCCTT	TGCTCACGTC	TCTCTGGCCC	ACTCATGATG	GAGAAGTGTG	5400
GTCAGAGGGG	AGCAATGGC	TTTGCTGCTT	ATGAGCACAG	AGGAATTCA	TCCCCAGGCA	5460
GCCCTGCCCT	TGACTCCAAG	AGGGTGAAGT	CCACAGAAGT	GAGCTCCTGC	CTTAGGGCCT	5520
CATTGCTCT	TCATCCAGGG	AACTGAGCAC	AGGGGGCCTC	CAGGAGACCC	TAGATGTGCT	5580
CGTACTCCCT	CGGCTGGGA	TTTCAGAGCT	GGAAATATAG	AAAATATCTA	GCCCAAAGCC	5640
TTCATTTAA	CAGATGGGA	AAAGTGAGCC	CCAAGATGGG	AAAGAACAC	ACAGCTAAGG	5700
GAGGGCCTGG	GGAGCCCCAC	CCTAGCCCT	GCTGCCACAC	CACATTGCCT	CAACAACCGG	5760
CCCCAGAGTG	CCCAGGCACT	CCTGAGGTAG	CTTCTGGAAA	TGGGGACAAG	TCCCCTCGAA	5820
GGAAAGGAAA	TGACTAGAGT	AGAATGACAG	CTAGCAGATC	TCTTCCCTCC	TGCTCCCAGC	5880
GCACACAAAC	CCGCCCTCCC	CTTGGTGTG	GCGGTCCCTG	TGGCCTTCAC	TTTGTTCACT	5940
ACCTGTCAGC	CCAGCCTGGG	TGCACAGTAG	CTGCAACTCC	CCATTGGTGC	TACCTGGCTC	6000
TCCTGTCCT	GCAGCTCTAC	AGGTGAGGCC	CAGCAGAGGG	AGTAGGGCTC	GCCATGTTTC	6060
TGGTGAGCCA	ATTGGCTGA	TCTTGGGTGT	CTGAACAGCT	ATTGGGTCCA	CCCCAGTCCC	6120
TTTCAGCTGC	TGCTTAATGC	CCTGCTCTCT	CCCTGGCCCA	CCTTATAGAG	AGCCCAAAGA	6180
GCTCCTGTAA	GAGGGAGAAC	TCTATCTGTG	TTTTATAATC	TTGCACGAGG	CACCAGAGTC	6240
TCCCTGGGTC	TTGTGATGAA	CTACATTAT	CCCCCTTCCT	GCCCCAACCA	CAAACCTCTT	6300
CCTTCAAAGA	GGGCCTGCCT	GGCTCCCTCC	ACCCAACACTGC	ACCCATGAGA	CTCGGTCAA	6360
GAGTCCATTG	CCCAGGTGGG	AGCCAACACTGT	CAGGGAGGTC	TTTCCCACCA	AACATTTTC	6420
AGCTGCTGGG	AGGTGACCAT	AGGGCTCTGC	TTTTAAAGAT	ATGGCTGCTT	CAAAGGCCAG	6480
AGTCACAGGA	AGGACTTCTT	CCAGGGAGAT	TAGTGGTGAT	GGAGAGGAGA	GTTAAAATGA	6540
CCTCATGTCC	TTCTGTCCA	CGGTTTTGTT	GAGTTTCAC	TCTTCTAATG	CAAGGGTCTC	6600
ACACTGTGAA	CCACTTAGGA	TGTGATCACT	TTCAAGGTGGC	CAGGAATGTT	GAATGTCTTT	6660
GGCTCAGTTC	ATTAAAAAAA	GATATCTATT	TGAAAGTTCT	CAGAGTTGTA	CATATGTTTC	6720
ACAGTACAGG	ATCTGTACAT	AAAAGTTCT	TTCTTAAACC	ATTCAACCAAG	AGCCAATATC	6780
TAGGCATTTT	CTTGGTAGCA	CAAATTTCT	TATTGCTTAG	AAAATTGTCC	TCCTTGTAT	6840
TTCTGTTTGT	AAGACTTAAG	TGAGTTAGGT	CTTTAAGGAA	AGCAACGCTC	CTCTGAAATG	6900
CTTGTCTTTT	TTCTGTTGCC	GAAATAGCTG	GTCCTTTTC	GGGAGTTAGA	TGTATAGAGT	6960
GTGGTATGT	AAACATTCT	TGTAGGCATC	ACCATGAACA	AAGATATATT	TTCTATTTAT	7020
TTATTATATG	TGCACTTCAA	GAAGTCACTG	TCAGAGAAAT	AAAGAATTGT	CTTAAATGTC	

SEQ ID NO:16 Protein sequence:  
Protein Accession #: XP\_051860.2

1	11	21	31	41	51	
MGAAGRQDFL	FKAMLTISWL	TLTCFPGATS	TVAAGCPDQS	PELQPWNPGH	DQDHVHIGQ	60
GKTLLLTSSA	TVYSIHISEG	GKLVIKDHD	PIVLRTRHIL	IDNGGELHAG	SALCPFQGNF	120
TIIILYGRADE	GIQPDPYYGL	KYIVGVKGGA	LELHGQKKLS	WTFLNKTLHP	GMMAEGGYFF	180
ERSWGHRGVI	VHVIDPKSGT	VIHSDRFDTY	RSKKESERLV	QYNNAVPDGR	ILSVAVNDEG	240
SRNLDDMARK	AMTKLGSKHF	LHLGFRHPWS	FLTVKGNPSS	SVEDHIEYHG	HRGSAARVF	300
KLFQTEHGEY	FNVSLSSSEWV	QDVEWTEWFD	HKVSQTKGG	EKISDLWKAH	PGKICNRPID	360
IQATTMDGVN	LSTEVVYKKG	QDYRFACYDR	GRACRSYRVR	FLCGKPVPRK	LTVTIDTNVN	420
STILNLEDNV	QSWKPGDTLV	IASTDYSMYQ	AEFQVLPCT	SCAPNQVKVA	GKPMYLHIGE	480
EIDGVDMRAE	VGLLSRNII	MGEAMEDKCY	YRNHICNFFD	FDTFGGHIFK	ALGFKAHLE	540
GTELKHMQQ	LVGQYPIHFH	LAGDVDERGG	YDPPTYIRD	SIHHTFSRCV	TVHGSNGLI	600
KDVGVYNSLG	HCFFTEDGPE	ERNTFDHCLG	LLVKGTL	SDRDSKMCKM	ITEDSYPGYI	660
PKPRQDCNAV	STFWMANPNN	NLINCAAAGS	EETGFWFIFH	HVPTGPSVGM	YSPGYSEHIP	720
LGKFYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPRAPI	780
IRHFIAYKNQ	DHGAWLRGGD	VWLDSRFAD	NGIGLTLASG	GTFPYDDGSK	QEIKNSLFVG	840
ESGNVGTEMM	DNRIWGPGL	DHSGRTPIG	QNFFPIRGQL	YDGPINIQNC	TFRKFVALEG	900
RHTSALAFRL	NNAQSCP	NVTGIAFEDV	PITSRVFFGE	PGPWFNQLDM	DGDKTSVFHD	960
VDGSVSEYPG	SYLKNDNW	VRHPDCINVP	DWRGAICSGC	YAQM	YIQAYK TSNLRM	1020
NDFPSHPLYL	EGALTRSTHY	QQYQPVVT	KGYTIHWDQT	APAELAIWLI	NFNKGDWIRV	1080

GLCYPRGTTF SILSDVHNRL LKQTSKTGVF VRTLQMDKVE QSYPGRSHYY WDEDGLLFL 1140  
 KLKAQNEREK FAFCSMKGCE RIKIKALIPK NAGVSDCTAT AYPKFTERAV DVVPMPKKLF 1200  
 GSQQLTKDHF LEVKMESSKQ HFFHLWNDFA YIEVDGKKYP SSEDGIQVVV IDGNQGRVVS 1260  
 HTSFRNSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRGLKLKE 1320  
 QMAFVGFKGS FRPIWVTLDT EDHKAKIFQV VPIPVVKKKK L

SEQ ID NO:17 DNA sequence

Nucleic Acid Accession #: NM\_015515.1  
Coding sequence: 61-1329

1	11	21	31	41	51	
AGTTCTGCGG	TGCCAGGGAG	TGGAGCAGAG	CTCAGCCCCG	TCCCAAACAC	AGATGGGACC	60
ATGAACCTCCG	GACACAGCTT	CAGCCAGACC	CCCTCGGCCT	CCTTCCATGG	CGCCGGAGGT	120
GGCTGGGGCC	GGCCCAGGAG	CTTCCCCAGG	GCTCCCACCG	TCCATGGCGG	TGCGGGGGGA	180
GCCCCGATCT	CCCTGTCCTT	CACCACGCCG	AGCTGCCAC	CCCCTGGAGG	GTCTTGGGGT	240
TCTGGAAGAA	GCAGCCCCCT	ACTAGGCGGA	AATGGGAAGG	CCACCATGCA	GAATCTCAAC	300
GACCGCCTGG	CCTCCCTACCT	GGAGAACGTT	CGCGCCCTGG	AGGAGGCCAA	CATGAAGCTG	360
GAAAGCCGCA	TCCTGAAATG	GCACCAGCAG	AGAGATCCTG	GCAGTAAGAA	AGATTATTCC	420
CAGTATGAGG	AAAACATCAC	ACACCTGCAG	GAGCAGATAG	TGGATGGTAA	GATGACCAAT	480
GCTCAGATT	TTCTTCTCAT	TGACAATGCC	AGGATGGCAG	TGGATGACTT	CAACCTCAAG	540
TATGAAAATG	AAACACTCCTT	TAAGAAAGAC	TTGGAAATTG	AAGTCGAGGG	CCTCCGAAGG	600
ACCTTAGACA	ACCTGACCAT	TGTCACAAACA	GACCTAGAAC	AGGAGGTGGA	AGGAATGAGG	660
AAAGAGCTCA	TTCTCATGAA	GGAGCACCAT	GAGCAGGAAA	TGGAGGAGCA	TCATGTGCCA	720
AGTGAATTCA	ATGTCATGT	GAAGGTGGAT	ACAGGTCCA	GGGAAGATCT	GATTAAGGTC	780
CTGGAGGATA	TGAGACAAGA	ATATGAGCTT	ATAATAAAGA	AGAACGATCG	AGACTTGGAC	840
ACTTGGTATA	AAGAACAGTC	TGCAGCCATG	TCCCAGGAGG	CAGCCAGTCC	AGCCACTGTG	900
CAGAGCAGAC	AAGGTGACAT	CCACGAACAT	AAGCGCACAT	TCCAGGCCCT	GGAGATTGAC	960
CTGCAGGCAC	AGTACAGCAC	GAAATCTGCT	TTGGAAAACA	TGTTATCCGA	GACCCAGTCT	1020
CGGTACTCCT	GCAAGCTCCA	GGACATGCAA	GAGATCATCT	CCCACTATGA	GGAGGAACTG	1080
ACGCAGCTAC	GCCACGAAC	GGAGCGGCAG	AACAAATGAAT	ACCAAGTGCT	GCTGGGCATC	1140
AAAACCCACC	TGGAGAAGGA	AATCACCAAG	TACCGACGGC	TCCTGGAGGG	AGAGAGTGAA	1200
GGGACACGGG	AAGAATCAA	GTCGAGCATG	AAAGTGTCTG	CAACTCCAAA	GATCAAGGCC	1260
ATAACCCAGG	AGACCATCAA	CGGAAGATTA	GTTCTTTGTC	AAGTGAATGA	AATCCAAAAG	1320
CACGCATGAG	ACCAATGAA	GTTTCCGCCT	GTTGTAAAGT	CTATTTCCC	CCAAGGAAAG	1380
TCCTTGCACA	GACACAGTG	AGTGAGTTCT	AAAAGATACC	CTTGGAAATTA	TCAGACTCAG	1440
AAACTTTTAT	TTTTTTTTT	CTGTAACAGT	CTCACCAAGAC	TTCTCATATA	GCTCTTAATA	1500
TATTGCACTT	TTCTAATCAA	AGTGCAGGTT	TATGAGGGTA	AAGCTCTACT	TTCTACTG	1560
AGCCTTCAGA	TTCTCATCAT	TTTGCATCTA	TTTGTAGCC	AATAAAACTC	CGCACTAGC	

SEQ ID NO:18 Protein sequence:

Protein Accession #: NP\_056330.1

1	11	21	31	41	51	
MNSGHFSQT	PSASFHGAGG	GWGRPRSFP	APTVHGGAGG	ARISLSFTTR	SCPPPGGSWG	60
SGRSSPLLLG	NGKATMQNLN	DRLASYLEKV	RALEEANMKL	ESRILKWHQQ	RDPGSKKDYS	120
QYEENITHLQ	EQIVDGKMTN	AQIILLIDNA	RMAVDDFNLK	YENEHSFKKD	LEIEVEGLRR	180
TLDNLNTIVTT	DLEQEVEGMR	KELILMKEHH	EQEMEEHHVP	SDFNVNVKVD	TGPREDLIK	240
LEDMRQEYEL	IICKKHDLD	TWYKEQSAAM	SQEAASPATV	QSRQGDIHEL	KRTFQALEID	300
LQAQYSTKSA	LENMLSETQS	RYSKLQDMQ	EIIISHYEEEL	TQLRHELERQ	NNEYQVLLGI	360
KTHLEKEITT	YRRLLEGES	GTREESKSSM	KVSATPKIKA	ITQETINGRL	VLCQVNEIQK	420
HA						

SEQ ID NO:19 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
TTTTTTTTTT	TTAAAAAAA	GAGGCTTGGT	AAGTTTTGA	TACTTAGTTG	ACTTTTAGCA	60
TTATCCAGCA	TTTGTTATTAT	GAACCAGTGA	GTACTGTAAT	TTTTCTTCC	CTTCAGAAA	120
GAACCAAAGG	GAACATATAA	ATGTTTCCA	TTTTNNNNN	NNNNNNNNNN	NNNNNNNNNN	180
NNNNACCCAT	CGTGCATGA	TCNNNNNNNN	NNNNNNNNNN	NNNNNTGGG	ATCCAGTTTC	240
AAATAAGGTA	TGGGAAAAAC	AGATGTTTC	ATTATGCCA	CTTAATCCTT	ACTTCCGATT	300
ATAATTATAC	ATGTTGGCT	GTAATAACTA	TACTAAAGCA	TGCTTGTGAA	AGTAGACTTC	360
TACAAGGACA	AAAAACCCAC	AACAACAAAG	ATCGATCACG	AAAGACAAGG	CATATTCAATT	420
CATTAATTAA	CTTCTCTTAG	ACCCGGGACA	TGTGGGACAA	ATACTTTGT	CCTCATGGAT	480
GGCTTGATAA	TTTATTATA	TGTTCTAGAG	TCTGAGGATT	TTCTTCAGT	GGCAGACAAAC	540
AAAGGATGTT	ACAATTACT	TCAAAATAAT	ACAATCATGG	TTTAATTAC	AGTGTAAATC	600
CATAACTATT	TTATAGAGAT	GGATTATCAT	ACATGGGATT	ATAAAATAA	CTTACCCATA	660
TGCTTGCAA	ATAGACTTT	CCTATTGGGA	GGAACATCTT	TTAACCTAAA	ACGGATTAT	720
TTCAGATGAA	TTAGACAGTA	CATTTTCAG	GAGAACCCAGC	CTTACTGGAT	GATCTTTGT	780
CAGGTTTGGG	GGCCTCTTCT	TTGTCTTGC	AACCATAACC	CCTTTTCAGC	TGAAGACACCAC	840
TGGCCTTCAA	CCCAAGCCAG	GAGTTGGCT	CAAATGA			

SEQ ID NO:20 DNA sequence

Nucleic Acid Accession #: D32051.1

Coding sequence: 72-1373

1	11	21	31	41	51	
GAATTGAAAC	CAGGTGGCCA	CCCGGTGTCG	GTTTCATTTT	CCTTTGGAAT	TTCTGCTTTA	60
CAGACAGAAC	AATGGCAGCC	CGAGTACTTA	TAATTGGCAG	TGGAGGAAGG	GAACATACGC	120
TGGCCTGGAA	ACTTGCACAG	TCTCATCATG	TCAAACAAGT	GTTGGTTGCC	CCAGGAAACG	180
CAGGCACTGC	CTGCTCTGAA	AAGATTTCAA	ATACCGCCAT	CTCAATCAGT	GACCACACTG	240
CCCTTGCTCA	ATTCTGCAA	GAGAAGAAAA	TTGAATTGT	AGTTGTTGGA	CCAGAAGCAC	300
CTCTGGCTGC	TGGGATTGTT	GGGAACCTGA	GGTCTGCAGG	AGTGCATG	TTTGGCCCAA	360
CAGCAGAACG	GGCTCAGTTA	GAGTCCAGCA	AAAGGTTTC	CAAAGAGTTT	ATGGACAGAC	420
ATGGAATCCC	AACCGCACAA	TGGAAGGCTT	TCACCAAACC	TGAAGAACCC	TGCAGCTTC	480
TTTGAGTGC	AGACTTCCCCT	GCTTTGGTTG	TGAAGGCCAG	TGGTCTTGCA	GCTGGAAAAG	540
GGGTGATTGT	TGCAAAGAGC	AAAGAAGAGG	CCTGCAAAGC	TGTACAAGAG	ATCATGCAGG	600
AGAAAGCCTT	TGGGGCAGCT	GGAGAAACAA	TTGTCATTGA	AGAACTTCTT	GACGGAGAAG	660
AGGTGTCGTG	TCTGTGTTTC	ACTGATGGCA	AGACTGTGGC	CCCCATGCC	CCAGCACAGG	720
ACCATAAGCG	ATTACTGGAG	GGAGATGGTG	GCCCTAACAC	AGGGGAATG	GGAGCCTATT	780
GTCCAGCCCC	TCAGGTTTCT	AATGATCTAT	TACTAAAAAT	TAAAGATACT	GTTCTTCAGA	840
GGACAGTGGA	TGGCATGCAG	CAAGAGGGTA	CTCCATATAC	AGGTATTCTC	TATGCTGGAA	900
TAATGCTGAC	CAAGAATGGC	CCAAAAGTTC	TAGAGTTAA	TTGCCGTTT	GGTGTATCCAG	960
AGTCCAAGT	AATCCCTCCA	CTTCTTAAA	GTGATCTTA	TGAAGTGATT	CAGTCCACCT	1020
TAGATGGACT	GCTCTGCACA	TCTCTGCTG	TTTGGCTAGA	AAACCACACC	GCCCTAACG	1080
TTGTCATGGC	AAGTAAAGGT	TATCCTGGAG	ACTACACCAA	GGGTGTAGAG	ATAACAGGGT	1140
TTCCTGAGGC	TCAAGCTCTA	GGACTGGAGG	TGTCCCATGC	AGGCACATGCC	CTCAAAATG	1200
GCAAAGTAGT	AACTCATGGG	GGTAGAGTTC	TTGCAGTCAC	AGCCATCCGG	GAAAATCTCA	1260
TATCAGCCCT	TGAGGAAGCC	AAGAAAGGAC	TAGCTGCTAT	AAAGTTTGAG	GGAGCAATT	1320
ATAGGAAAGA	CATCGGCTT	CGTCCATAG	CTTCCTCCA	GCAGCCCAGG	TAAAACCTCA	1380
AGCAAGTTAG	CTGTAGTGCC	ATTCAGAAA	CTGGCCTAAA	TGGCTATGTA	GAACATTCCA	1440
TTAACCCCTAT	AAGTCATTCA	GTATTCTTT	CTCTCTGTGG	GAGTGATACA	GTCTGGTTT	1500
GTATTTGTT	TGAATCAAA	CTGGTTATAG	CAATACTCAA	ATGGAAAAAA	CTTCATGATA	1560
GCGTAAGTTT	GGAAAGTTA	GCAAAATCAC	AGTGGTACTG	ATTTTATT	GTGTTCTATT	1620
TTTTTATT	TATATTTTA	ATTTTTTAA	CAGGGTCTTC	CTCTCTCGCC	CAAGTTCTCA	1680
TGCCTCAGCC	TCCCAAATAG	CTGGGACTAC	AGGCACAGGC	CACCAACACT	GGCTAATT	1740
TTTGTATT	TTGTGGAGAT	GGGGTTCA	ATGTTGCCAA	GGCCAGTCTG	AAAGCCTGGG	1800
CTCAAGTGAT	CCTCCTGCTT	TGGCCTCCCA	AAATGCTGGG	ACTATAGGCA	TGAGGCGCTG	1860
CACTTGGCCT	GATACTGATT	TTTATTCC	GGCTTATCAC	ATAGTGTGT	ATTTGAAACA	1920
TAGTTCATGG	TTTTATCAAA	GAACGTGAAGA	TGAGAATACT	GGTCATCTAA	CTTTGTAATT	1980

TGATTTGATT ATACTGTAAA GTTTGACAGT CCCATTTAA CCTGCCTTG TATCTATTAC 2040  
 TAAAATGTAT TTTTGACCT CTTACTGATT CATGGTTGGT ATGTACAAAC TGTTGACTTG 2100  
 TAAAATCAAT AAAGTCTTAG TTGG

SEQ ID NO:21 Protein sequence:  
 Protein Accession #: BAA06809.1

1	11	21	31	41	51	
MAARVLIIGS	GGREHTLAWK	LAQSHHVQV	LVAPGNAGTA	CSEKISNTAI	SISDHTALAQ	60
FCKEKKIEFV	VVGPEAPLAA	GIVGNLRSAG	VQCFGPTAEA	AQLESSKRFA	KEFMDRHGIP	120
TAQWKAFTKP	EEACSFILSA	DFPALVVKAS	GLAAGKGIV	AKSKEEACKA	VQEIMQEKAF	180
GAAGETIVIE	ELLDGEEVSC	LCFTDGKTV	PMPPAQDHKR	LLEGDGGPNT	GGMGAYCPAP	240
QVSNDLLKI	KDTVLQRTVD	GMQQEGTPYT	GILYAGIMLT	KNGPKVLEFN	CRFGDPECQV	300
ILPLLKSDLY	EVIQSTLDGL	LCTS LPVWLE	NHTALTVVMA	SKGYPGDYTK	GVEITGFPEA	360
QALGLEVSHA	GTALKNGKVV	THGGRVLAVT	AIRENLISAL	EEAKKGLAAI	KFEGAIYRKD	420
IGFRAIAFLQ	QPR					

SEQ ID NO:22 DNA sequence  
 Nucleic Acid Accession #: EOS cloned  
 Coding sequence: 1-2424

1	11	21	31	41	51	
ATGCCCCCTT	TCCTGTTGCT	GGAGGCCGTC	TGTGTTTCC	TGTTTCCAG	AGTGCCCCCA	60
TCTCTCCCTC	TCCAGGAAGT	CCATGTAAGC	AAAGAAACCA	TCGGGAAGAT	TTCAGCTGCC	120
AGCAAAATGA	TGTGGT GCTC	GGCTGCAGTG	GACATCATGT	TTCTGTTAGA	TGGGTCTAAC	180
AGCGTCGGGA	AAGGGAGCTT	TGAAAGGTCC	AAGCACTTG	CCATCACAGT	CTGTGACGGT	240
CTGGACATCA	GCCCCGAGAG	GGTCAGAGTG	GGAGCATTCC	AGTTCAGTT	CACTCCTCAT	300
CTGGAATTCC	CCTTGGATT	ATTTCAACC	CAACAGGAAG	TGAAGGCAAG	AATCAAGAGG	360
ATGGTTTCA	AAGGAGGGCG	CACGGAGACG	GAACTTGCTC	TGAAATACCT	TCTGCACAGA	420
GGGTTGCCTG	GAGGCAGAAA	TGCTTCTGTG	CCCCAGATCC	TCATCATCGT	CACTGATGGG	480
AACTCCCAGG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
TTTGCTGTGG	GGGT CAGGTT	TCCCAGGTGG	GAGGAGCTGC	ATGCACTGGC	CAGCGAGCCT	600
AGAGGGCAGC	ACGTGCTGTT	GGCTGAGCAG	GTGGAGGATG	CCACCAAACGG	CCTCTTCAGC	660
ACCCCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
CCCTGTGAGC	ACAGGACGCT	GGAGATGGTC	CGGGAGTTCG	CTGGCAATGC	CCCATGCTGG	780
AGAGGATCGC	GGCGGACCC	TGCGGTGCTG	GCTGCACACT	GTCCTTCTA	CAGCTGGAAG	840
AGAGTGTTC	TAACCCACCC	TGCCACCTGC	TACAGGACCA	CCTGCCAGG	CCCCTGTGAC	900
TCGCAGCCCT	GCCAGAATGG	AGGCACATGT	GTTCCAGAAG	GACTGGACGG	CTACCA GTGC	960
CTCTGCCCGC	TGGCCTTGG	AGGGGAGGCT	AACTGTGCC	TGAAGCTGAG	CCTGGAATGC	1020
AGGGTCGACC	TCCTCTTCC	GCTGGACAGC	TCTGCGGGCA	CCACTCTGGA	CGGCTTCTG	1080
CGGGCCAAG	TCTTCGTGAA	CGGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
CGAGTGGGTG	TGCCACATA	CAGCAGGGAG	CTGCTGGTGG	CGGTGCCTGT	GGGGGAGTAC	1200
CAGGATGTGC	CTGACCTGGT	CTGGAGCCTC	GATGGCATT	CCTTCCGTGG	TGGCCCCACC	1260
CTGACGGGCA	GTGCCCTGCG	GCAGGCGCA	GAGCGTGGCT	TCGGGAGCGC	CACCAAGGACA	1320
GGCCAGGACC	GGCCACGTAG	AGTGGTGGTT	TTGCTCACTG	AGTCACACTC	CGAGGATGAG	1380
GTTGCGGGCC	CAGCGCGTC	CGCAAGGGCG	CGAGAGCTGC	TCCTGCTGGG	TGTAGGCAGT	1440
GAGGCCGTGC	GGGCAGAGCT	GGAGGAGATC	ACAGGCAGCC	CAAAGCATGT	GATGGTCTAC	1500
TCGGATCCTC	AGGATCTGTT	CAACCAAATC	CCTGAGCTGC	AGGGGAAGCT	GTGCAGCCGG	1560
CAGCGGCCAG	GGTGCCGGAC	ACAAGCCCTG	GACCTCGTCT	TCATGTTGGA	CACCTCTGCC	1620
TCAGTAGGGC	CCGAGAATT	TGCTCAGATG	CAGAGCTTTG	TGAGAAGCTG	TGCCCTCCAG	1680
TTTGAGGTGA	ACCCTGACGT	GACACAGGTC	GGCCTGGTGG	TGTATGGCAG	CCAGGTGCGAG	1740
ACTGCCTTCG	GGCTGGACAC	CAAACCCACC	CGGGCTGC	TGCTGCGGGC	CATTAGCCAG	1800
GCCCCCTACC	TAGGTGGGT	GGGCTCAGCC	GGCACCGCCC	TGCTGCACAT	CTATGACAAA	1860
GTGATGACCG	TCCAGAGGGG	TGCCC GGCC	GGTGTCCCCA	AAGCTGTGGT	GGTGCTCAC	1920
GGCGGGAGAG	GCAGCAGAGGA	TGCAGCGTT	CCTGCCAGA	AGCTGAGGAA	CAATGGCATT	1980
TCTGTCTTGG	TCGTGGCGT	GGGGCCTGTC	CTAAGT GAGG	GTCTGCGGAG	GCTTGCAAGT	2040
CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGACGTG	2100

CTCATTGAGT GGCTGTGTGG AGAAGCCAAG CAGCCAGTCA ACCTCTGCAA ACCCAGCCCC 2160  
 TGCATGAATG AGGGCAGCTG CGTCCTGCAG AATGGGAGCT ACCGCTGCAA GTGTCGGGAT 2220  
 GGCTGGGAGG GCCCCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280  
 CAGGGATGGA TTCTTGAGAC GCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC 2340  
 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400  
 AATGTCTGTG CCCCAGGTCC TTAG

SEQ ID NO:23 Protein sequence:  
 Protein Accession #: EOS cloned

1	11	21	31	41	51	
MPPFLLLEAV	CVFLFSRVPP	SLPLQEVHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
SVGKGSFERS	KHFAITVCVG	LDISPERVRV	GAFQFSSTPH	LEFPLDSFST	QQEVKARIKR	120
MVFKGGRTE	ELALKYLLHR	GLPGGRNASV	PQILIIIVTDG	KSQGDVALPS	KQLKERGVTV	180
FAVGVRFPRW	EELHALASEP	RQHQHVLLEAQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
PCEHRTLEMV	REFAGNAPCW	RGSRRRTLAVL	AHCPCFYSWK	RVFLTHPATC	YRTTCPGPCD	300
SQPCQNGGTC	VPEGLDGYQC	LCPLAFIGGEA	NCALKLSLEC	RVDLLFLLDS	SAGTTLDGFL	360
RAKVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPDLVWSL	DGIPFRGGPT	420
LTGSALRQAA	ERGFGSATRT	GQDRPRVVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
EAVRAELEEI	TGSPKHVMVY	SDPQDLFNQI	PELQGKLCR	QRPGCRTQAL	DLVFMLDTSA	540
SVGPNENFAQM	QSFVRSCALQ	FEVNPDVTQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAB	PAQKLRNNGI	660
SVLVVGVPV	LSEGRLLAG	PRDSLHVA	YADLRYHQDV	LIEWLCGEAK	OPVNLCKPSP	720
CMNEGSCVLIQ	NGSYRCKRD	GWEGPHCENR	EWSSCSVCVS	QGWILETPLR	HMAPVQEGSS	780
RTPPSNYREG	LGTEMVPTFW	NVCAPGP				

SEQ ID NO:24 DNA sequence  
 Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
AGGTCGGCTG	GTTATCGGGG	GTTGGAGGGC	TGAGGTCGGG	AGGGTGGTGT	GTACAGAGCT	60
CTAGGACTCA	CGCACCAAGC	CAGTCGGGG	TTTTGGGCCG	AGGCCTGGGT	TACAAGCAGC	120
AAGTGCAGGG	TTGGGCCAC	TGCGAGGCCG	TTTAGAAAA	CTGTTAAAAA	CAAAGAGCAA	180
TTGATGGATA	AATCAGGAAT	AGATTCTCTT	GACCATGTGA	CATCTGATGC	TGTGGAACCTT	240
GCAAATCGAA	GTGATAACTC	TTCTGATAGC	AGCTTATTAA	AAACTCAGTG	TATCCCTTAC	300
TCACCTAAAG	GGGAGAAAAG	AAACCCATT	CGAAAATTG	TTCGTACACC	TGAAAGTGT	360
CACGCAAGTA	TTCATCAAGT	GACTCATCTT	TTGAACCAGT	ACCATTGACT	ATAAAAGCTA	420
TTTTTGAAAG	ATTCAAGAAC	AGGAAAAGA	GATATAAAAA	AAAGAAAAG	AGGAGGTACC	480
AGCCAACAGG	AAGACCACGG	GGAAAGACAG	AAGGAAGGAG	AAATCCTATA	TACTCACTAA	540
TAGATAAGAA	GAAACAATT	AGAACAGAG	GATCTGGCTT	CCCATTTTA	GAATCAGAGA	600
ATGAAAAAAA	CGCACCTTG	AGAAAATT	TAACGTTGA	GCAAGCTGTT	GCAAGAGGAT	660
TTTTTAAC	TATTGAAAAA	CTGAAGTATG	AACACCACCT	GAAAGAATCA	TTGAAGCAA	720
TGAATGTTGG	TGAAGATT	GAAAATGAAG	ATTTGACAG	TCGTAGATAC	AAATTTTTGG	780
ATGATGATGG	ATCCATTCT	CCTATTGAGG	AGTCAACGCT	TTTATCTTGA	GGACATGGTG	840
TCTGGAGTTA	AAGGTATTGG	CATACTCCAC	ACATCTGTAC	CATTCTTGAG	TGATCGCTTA	900
GBAATGAATG	TGATTGGAC	TCATTCTATG	ATGAGAGTAA	GCAATGCTTT	TTTTCCAGG	960
GTGTCAAATT	GAGAACCGAG	TAGATCCCCA	CCACCTACAG	AAAAAAGGAC	CCTAAAGTAA	1020
ATTGGTTGAA	GAAATTAGAT	CCCAAAGATT	CTTGGTGAAT	TTTGAAGTCT	TCATCAGTAT	1080
ATCCATATT	AAAGCAGATG	ACAGAACCCA	AAAGTAATTAT	GGGCTGACAG	GACAACGTGA	1140
TCAGTTTCAT	AAAAAAGGGC	AAACTTGAAG	ATAAATCTTT	TGACTCCAGC	TCTTAGAGG	1200
ATCTAAAGTG	ACCTTGATGG	ACAGTGGAAAG	AAATCACAAC	ATGGAATTCC	TCGAATAACA	1260
ATTTATTGAC	TTTAAATAAT	TTTGCTTAAT	GCTACATATA	CACAATTAAA	AAACCTTAC	1320
ACTATTTCTA	GAAAGTCAGC	ATGTATTTT	GGCTCGAAGT	TTCTCTAGTG	TTTCTGTGG	1380
AAGGAATAAA	AATTGAGGT	TTCAATACAA	AAACAAAACA	AAACACACGA	AACACGAAA	1440
ACAATCTGTT	GTGCGGCGCC	CCTGGGCC	TTGAGAGAAA	ACTTTTTAGA	ACCCCTTTG	1500
CGTTGTGGCG	GCCCCGGGGC	CCCACAGTTG	GGTTTAGGTG	GGCACCTTG	TGTCTACAAG	1560
TGGTGTCTCC	CCAAGAGAGA	GAACACCTCC	GGGGTCAAGC	GGACAAACAAG	AGTGCCTCGT	1620

GAGGACTCTT CACCCAAAGT ATATAAAACC CGCCCCGGG GGGAACCAAC GGCGCTTTT 1680  
 CTGTAGACAC AACCCCCACA GTGGGAACCT CTGAGGGCGC ACACACAGGG CGAGCCTAT 1740  
 CAACAAGGGG TGCCCAACAG AAACCCCGAG TTAAAAATCG

SEQ ID NO:25 DNA sequence  
 Nucleic Acid Accession #: BC001972.1  
 Coding sequence: 183-1019

1	11	21	31	41	51	
GGTCGGCTGG	TTATCGGGAG	TTGGAGGGCT	GAGGTCGGGA	GGGTGGTGTG	TACAGAGCTC	60
TAGGACTCAC	GCACCAGGCC	AGTCGCGGGT	TTTGGGCCGA	GGCCTGGGTT	ACAAGCAGCA	120
AGTGCAGGGT	TGGGCCACT	GCGAGGCCGT	TTTAGAAAAC	TGTTTAAAAC	AAAGAGCAAT	180
TGATGGATAA	ATCAGGAATA	GATTCTCTTG	ACCATGTGAC	ATCTGATGCT	GTGGAACTTG	240
CAAATCGAAG	TGATAACTCT	TCTGATAGCA	GCTTATTTAA	AACTCAGTGT	ATCCCTTACT	300
CACCTAAAGG	GGAGAAAAGA	AACCCCATTG	AAAAATTGTT	TCGTACACCT	GAAAGTGTTC	360
ACGCAAGTGA	TTCATCAAGT	GACTCATCTT	TTGAACCAAT	ACCATTGACT	ATAAAAGCTA	420
TTTTTGAAG	ATTCAAGAAC	AGGAAAAAAGA	GATATAAAA	AAAGAAAAAG	AGGAGGTACC	480
AGCCAACAGG	AAGACCACGG	GGAAGACCGAG	AAGGAAGGAG	AAATCCTATA	TACTCACTAA	540
TAGATAAGAA	GAAACAATTG	AGAACAGAG	GATCTGGCTT	CCCATTTTA	GAATCAGAGA	600
ATGAAAAAAA	CGCACCTTGG	AGAAAAATTG	TAACGTTGAA	GCAAGCTGTT	GCAAGAGGAT	660
TTTTTAACTA	TATTGAAAAA	CTGAAGTATG	AAACACCACCT	GAAAGAATCA	TTGAAGCAAA	720
TGAATGTTGG	TGAAGATTG	GAAAATGAAG	ATTTTGACAG	TCGTAGATAC	AAATTTTGG	780
ATGATGATGG	ATCCATTCT	CCTATTGAGG	AGTCAACAGC	AGAGGATGAG	GATGCAACAC	840
ATCTTGAAGA	TAACGAATGT	GATATCAAAT	TGGCAGGGGA	TAGTTTCATA	GTAAGTTCTG	900
AATTCCCTGT	AAGACTGAGT	GTATACTTAG	AAGAACAGGA	TATTACTGAA	GAAGCTGCTT	960
TGTCTAAAAA	GAGAGCTACA	AAAGCCAAA	ATACTGGACA	GAGAGGCCGT	AAAATGTGAC	1020
AGGATCATGA	ATGTCAAAGG	CTTTTATCTT	GAGAACATGG	TGTCTGGAGT	TAAGGACTA	1080
TTGTTAGATC	TGTGGGAAGG	AATTACAAGA	CAGTTGCTAA	AAGTTGAAA	AAAGACGGTTG	1140
CTAAACGTTA	TGAAAAAACCA	GATAATCTAC	TTTTTTACCT	TAGGTATTGG	CATACTCCAC	1200
ACATCTGTAC	CATTCTTGAG	TGATCGCTT	GGAAATGAATG	TGATTTGAAC	TCATTATGTT	1260
TGAGAGGGTG	TCAAATTGAG	AACCAGGTAG	ATCCCCACCA	CCTACAGTAA	AAAGGACCT	1320
AAAGTAAATT	GGTTGAAGAA	ATTAGATCCC	AAAGATTCTT	GGTGAATTTC	GAAGTCTTCA	1380
TCAGTATATC	CATATTTAAA	CGAGATGACA	GAAGCCAAAG	TAATTATGGG	CTGACAGGAC	1440
AACTGGATCA	GTTTCATTAA	AAAGGGCAA	CTTGAAGATA	AATCTTTGA	CTCCAGCTCT	1500
TTAGAGGATC	TAAAGTGACC	TTGATGGACA	GTGGAAGAAA	TCACAAACATG	GAATTCCCTCG	1560
AATAACAATT	TATTGACTTT	AAATAATTGCT	GTCTAATGCT	ACATATACAC	AATTAAAAAA	1620
CCTTACACT	AAAAAA	AAAAAA				

SEQ ID NO:26 Protein sequence:  
 Protein Accession #: AAH01972.1

1	11	21	31	41	51	
MDKSGIDSLS	HVTSDAVELA	NRSDNSSDSS	LFKTQCIPYS	PKGEKRNPPIR	KFVRTPESVH	60
ASDSSSDSSF	EPIPLTIKAI	FERFKNRKKR	YKKKKRRYQ	PTGRPRGRPE	GRRNPIYSLI	120
DKKKQFRSRG	SGFPFLESEN	EKNAPWRKIL	TFEQAVERGF	FNYIEKLKYE	HHLKESLKQM	180
NVGEDLENED	FDSRRYKFLD	DDGSISPIEE	STADEDATH	LEDNECDIKL	AGDSFIVSSE	240
FPVRLSVYLE	EEDITEEAAL	SKKRATKAKN	TGQRGLKM			

SEQ ID NO:27 DNA sequence  
 Nucleic Acid Accession #: AK027016  
 Coding sequence: 207-1043

1	11	21	31	41	51	
CTTTTCTTCC	GCACGGTTGG	AGGAGGTCGG	CTGGTTATCG	GGAGTTGGAG	GGCTGAGGTC	60
GGGAGGGTGG	TGTGTACAGA	GCTCTAGGAC	TCACGCACCA	GGCCAGTCGC	GGATTTGGG	120

CCGAGGCCTG	GGTTACAAGC	AGCAAGTGC	CGGTTGGGGC	CACTGCGAGG	CCGTTTTAGA	180
AAACTGTTA	AAACAAAGAG	CAATTGATGG	ATAAATCAGG	AATAGATTCT	CTTGACCATG	240
TGACATCTGA	TGCTGTGGAA	CTTGCAAATC	GAAGTGATAA	CTCTTCTGAT	AGCAGCTTAT	300
TTAAAACCTCA	GTGTATCCCT	TACTCACCTA	AAGGGGAGAA	AAGAAACCCC	ATTCGAAAAT	360
TTGTTCGTAC	ACCTGAAAGT	GTTCACGCAA	GTGATTCATC	AAGTGACTCA	TCTTTGAAC	420
CAATACCAT	GACTATAAAA	GCTATTITG	AAAGATTCAA	GAACAGGAAA	AAGAGATATA	480
AAAAAAAGAA	AAAGAGGAGG	TACCAGCCAA	CAGGAAGACC	ACGGGGAAAGA	CCAGAAGGAA	540
GGAGAAATCC	TATATACTCA	CTAATAGATA	AGAAGAAACA	ATTTAGAAGC	AGAGGATCTG	600
GCTTCCCATT	TTTAGAATCA	GAGAATGAAA	AAAACGCACC	TTGGAGAAAA	ATTTAACGT	660
TTGAGCAAGC	TGTTGCAAGA	GGATTTTTA	ACTATATTGA	AAAGCTGAAG	TATGAACACC	720
ACCTGAAAGA	ATCATTGAAG	CAAATGAATG	TTGGTGAAGA	TTTAGAAAAT	GAAGATTTG	780
ACAGTCGTAG	ATACAAATT	TTGGATGATG	ATGGATCCAT	TTCTCCTATT	GAGGAGTCAA	840
CAGCAGAGGA	TGAGGATGCA	ACACATCTT	AAGATAACGA	ATGTGATATC	AAATTGGCAG	900
GGGATAGTT	CATAGTAAGT	TCTGAATTCC	CTGTAAGACT	GAGTGTATAC	TTAGAAGAAG	960
AGGATATTAC	TGAAGAAGCT	GCTTGTCTA	AAAAGAGAGC	TACAAAAGCC	AAAATACTG	1020
GACAGAGAGG	CCTGAAATG	TGACAGGATC	ATGAATGTCA	AAGGCTTTA	TCTTGAGAAC	1080
ATGGTGTCTG	GAGTAAAGG	TATTGGCATA	CTCCACACAT	CTGTACCAT	CTTGAGTGT	1140
CGCTTAGGAA	TGAATGTGAT	TTGAACTCAT	TCATGTTGAG	AGGGTGTCAA	ATTGAGAACCC	1200
AGGTAGATCC	CCACCAACCTA	CAGTAAAAAG	GACCCCTAAAG	TAAATTGGTT	GAAGAAATTAA	1260
GATCCCAAAG	ATTCTGGTG	AATTTGAAG	TCTTCATCAG	TATATCCATA	TTAAAACGAG	1320
ATGACAGAAAG	CCAAAGTAAT	TATGGCAAGT	AATGGTTTTT	ATCTTAACTA	TAAGTTATT	1380
GCTCAAGGGT	GTAATGGTCA	TTACCAAGGC	TTTTAGAATG	CAGTTCTCA	TTTGCTGTGG	1440
ACATGACCAT	AAAAAAAAT	TTCCCAGTAG	GTTCCTATC	TGCTACGTTG	CTAGCAATCA	1500
GCTTATTGGG	AACAGTTGAT	TAACTGTAAT	AGAAATGCAA	TACAAATAAA	ATGTGAACCA	1560
CATGTGATT	TTCTTAAAAA	TCAGTGAGAT	TTGAAAATTC	TCCTAGATCT	CTTGAAATCAT	1620
GCAAATTG	TTTGCCTTTA	TATTGTAACC	CTTGTGGGTT	GCTAATAACC	AAGCAGTTTG	1680
TAGTAGAGTT	AACTCAGGCT	CGTTCTAGGG	ACTCATTCA	GTTCACTCAC	TGTACACTCA	1740
TCTCTGGAAA	TGTAAAATT	ACTTTATAC	TATTGTTATG	AGGGCTGAC	AGGACAAC	1800
GATCAGTTTC	ATTAAGG	TATGTATGCA	TTAGAAAAGA	CATTTGTATG	GGTCATTCA	1860
AAGAGGGCTT	ATGAGGCTGT	GAAACCCAGA	GCTCTTAACG	CTGTGACCAA	AGATGGAAGT	1920
TCTCTATAGG	AAGCCATAGC	ACTCCTAATG	TTTGGTGTCA	TGTTTCCCTG	AGGAGATATA	1980
AAACGTAATA	ATCCATGATT	GTTGCCATGT	GAGAGTTTA	AAGGTTAAC	AAAATTCTC	2040
TTCTTCAGGG	CAAACCTGAA	GATAAACTT	TTGACTCCAG	CTCTTAGAG	GATCTAAAGT	2100
GACCTTGATG	GACAGTGGAA	GAAATCACAA	CATGGAATTC	CTCGAATAAC	AATTATTGAA	2160
CTTTAAATAA	TTTTGTCTAA	TGCTACATAT	ACACAATTAA	AAAACCTTA	CACTATTCT	2220
AGAAAGTCAG	CATGTATT	TGGCTCGAAG	TTTCTCTAGT	GTTTCTGTG	GAAGGAATAA	2280
AAATTGAGT	TTCAAAAAAA	AAAAAA	AAAAAA	AAAAAA	AAAAAA	

SEQ ID NO:28 Protein sequence:  
Protein Accession #: BAB15628.1

1	11	21	31	41	51	
MDKSGIDS	HVTSDAVELA	NRSDNSSDSS	LFKTQCIPYS	PKGEKRNP	KFVRTPESVH	60
ASDSSSDSSF	EPIPLTIKAI	FERFKNRKKR	YKKKKKRRYQ	PTGRPRGRPE	GRRNPIYSLI	120
DKKKQFRSRG	SGFPFLESEN	EKNAPWRKIL	TFEQAVALGF	FNYIEKLKYE	HHLKESLKQM	180
NVGEDLENED	FDSRRYKFLD	DDGSISPIEE	STAEDEDATH	LEDNECDIKL	AGDSFIVSSE	240
FPVRLSVYLE	EEDITEAAL	SKKRATKAKN	TGQRGLKM			

SEQ ID NO:29 DNA sequence  
Nucleic Acid Accession #: NM\_004289.3  
Coding sequence: 493-1695

1	11	21	31	41	51	
GCCGCCGCCT	CGTCCACCGG	AGGAGCCGGC	GCCAGCGTGG	ACGGCGGCAG	CCAGGCTGTG	60
CAGGGGGCG	CGGGGGACCC	CCGAGCGGCT	CGGAGTGGCC	CCTTGGACGC	CGGGGAAGAG	120
GAGAAGGCAC	CCGCGGAACC	GACGGCTAG	GTGCCGGACG	CTGGCGGATG	TGCGAGCGAG	180
GAGAATGGGG	TACTAAGAGA	AAAGCACGAA	GCTGTGGATC	ATAGTCCCA	GCATGAGGAA	240

AATGAAGAAA	GGGTGTCAGC	CCAGAAGGAG	AACTCACTTC	AGCAGAATGA	TGATGATGAA	300
AACAAAATAG	CAGAGAAACC	TGACTGGAG	GCAGAAAAGA	CCACTGAATC	TAGAAATGAG	360
AGACATCTGA	ATGGGACAGA	TACTTCTTTC	TCTCTGGAAG	ACTTATTCCA	GTTGCTTCA	420
TCACAGCCTG	AAAATTCACT	GGAGGGCATC	TCATTGGGAG	ATATT CCTCT	TCCAGGCAGT	480
ATCAGTGATG	GCATGAATTC	TTCAGCACAT	TATCATGTAA	ACTTCAGCCA	GGCTATAAGT	540
CAGGATGTGA	ATCTTCATGA	GGCCATCTTG	CTTGTCCCCA	ACAATACATT	TAGAAGAGAT	600
CCAACAGCAA	GGACTTCACA	GTCACAAGAA	CCATTCTGTC	AGTTAAATTTC	TCATACCACC	660
AATCCTGAGC	AAACCCCTCC	TGGAACTAAT	TTGACAGGAT	TTCTTCACC	GGTTGACAAT	720
CATATGAGGA	ATCTAACAAAG	CCAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTGAT	780
GAGATAAACT	TAATGTCATT	GGCCACAGAA	GACAACHTTG	ATCCAATCGA	TGTTTCTCAG	840
CTTTTGATG	AACCAGATTG	TGATTCTGGC	CTTCTTTAG	ATTCAAGTCA	CAATAATACC	900
TCTGTCATCA	AGTCTAATTG	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
ACTGACCAGT	AATCTAGTTG	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
GAACCCAGTA	AGCTTTGTCA	CTTGGATCAA	AGTGATTCTG	ATTTCCATGG	AGATCTTACA	1080
TTTCAACACG	TATTTCATAA	CCACACTTAC	CACTTACAGC	CAACTGCACC	AGAATCTACT	1140
TCTGAACCTT	TTCCGTGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CCTTGAAGAC	1200
ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTTGCATAT	CCCTTTTCT	1260
GTAGATGAAA	TTGTCGGCAT	GCCTGTTGAT	TCTTCAATA	GCATGTTAAG	TAGATATTAT	1320
CTGACAGACC	TACAAGTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
GCTGCGCAGA	ACTGTCGTA	ACGCAAATTG	GACATAATT	TGAATTAGA	AGATGATGTA	1440
TGTAACCTGC	AAGCAAAGAA	GGAAACTCTT	AAGAGAGAGC	AAGCACAATG	TAACAAAGCT	1500
ATTAACATAA	TGAAACAGAA	ACTGCATGAC	CTTATCATG	ATATTTTAG	TAGATTAAGA	1560
GATGACCAAG	GTAGGCCAGT	CAATCCCAAC	CACTATGCTC	TCCAGTGTAC	CCATGATGGA	1620
AGTATCTG	TAGTACCCAA	AGAACTGGT	GCCTCAGGCC	ACAAAAAGGA	AACCCAAAAG	1680
GGAAAGAGAA	AGTGAGAAGA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTTCA	1740
GAAACTGATT	ATTTGGATCA	GAAACCATTG	AAACTGCTTC	AAGAATTGTA	TCTTTAAGTA	1800
CTGCTACTTG	AATAACTCAG	TTAACGCTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
CTTCAAGATC	ACACTTGTGG	GCAATCTGGG	GGAGCCACAA	CTTTTCATGA	AGTGCATTGT	1920
ATACAAAATT	CATAGTTATG	TCCAAAGAAT	AGGTTAACAT	GAAAACCCAG	TAAGACTTTC	1980
CATCTGGCA	GCCATCCTT	TTAAGAGTAA	GTTGGTTACT	TCAAAAAGAG	CAAACACTGG	2040
GGATCAAATT	ATTTTAAGAG	GTATTTCACT	TTTAAATGCA	AAATAGCCTT	ATTTTCATT	2100
AGTTTGTAG	CACTATAGTG	AGCTTTCAA	ACACTATT	AATCTTATA	TTTAACATT	2160
AAATTTGCT	TTCT					

SEQ ID NO:30 Protein sequence:  
Protein Accession #: NP\_004280

1	11	21	31	41	51	
MNSSAHYHVN	FSQAIISQDVN	LHEAILLCPN	NTFRRDPTAR	TSQSQEPLFLQ	LNSHTTNPEQ	60
TLPGTNLTGF	LSPVDNHMRN	LTSQDLLYDL	DINIFDEINL	MSLATEDNFD	PIDVSQLFDE	120
PDSDSGLSLD	SSHNNNTSVIK	SNSSHSVCD	GAIGYCTDHE	SSSHHDLEGA	VGGYYPEPSK	180
LCHLDQSDSD	FHGDLTFQHV	FHNHTYHLQP	TAPESTSEPF	PWPGKSQKIR	SRYLEDTDRN	240
LSRDEQRAKA	LHIPFSVDEI	VGMPVDSFNS	MLSRYYLTDL	QVSLIRDIRR	RGKNKVAQN	300
CRKRKLDIIL	NLEDDVCNLQ	AKKETLKREQ	AQCNKAINIM	KQKLHDLYHD	IFSRLRDDQG	360
RPVNPNHYAL	QCTHDGSIL	VPKELVASGH	KKETQKGKRK			

SEQ ID NO:31 DNA sequence  
Nucleic Acid Accession #: NM\_033260.1  
Coding sequence: 1-1208

1	11	21	31	41	51	
ATGAAGTTGG	AGGTGTTCGT	CCCTCGCGCG	GCCCACGGGG	ACAAGCAGGG	CAGTGACCTG	60
GAGGGCGCGG	CGGGCAGCGA	CGCGCCGTCC	CCGCTGTCGG	CGGGCGGAGA	CGACTCCCTG	120
GGCTCAGATG	GGGACTGCGC	GGCCAAGCCG	TCCGCGGGCG	CGGGCGCCAG	AGATACGCAG	180
GGCGACGGCG	AACAGAGTGC	GGGAGGGCGG	CCGGGCGCGG	AGGAGGGCGAT	CCCGGCAGCA	240
GCTGCTGCAG	CGGTGGTGGC	GGAGGGCGCG	GAGGCCGGGG	CGGGCGGGCC	AGGCGCGGGC	300
GGCGCGGGGA	CGGGCGAGGG	TGCACGCAGC	AAGCCATATA	CGCGCGGGCC	CAAGCCCCCC	360

TACTCGTACA	TCGCGCTCAT	CGCCATGGCC	ATCCGCGACT	CGGCGGGCGG	GCGCTTGACG	420
CTGGCGGAGA	TCAACGAGTA	CCTCATGGC	AAGTTCCCCT	TTTTCGGCGG	CAGCTACACG	480
GGCTGGCGCA	ACTCCGTGCG	CCACAACCTT	TCGCTCAACG	ACTGCTTCGT	CAAGGTGCTG	540
CGCGACCCCT	CGCGGCCCTG	GGGCAAGGAC	AACTACTGGA	TGCTCAACCC	CAACAGCGAG	600
TACACCTTCG	CCGACGGGGT	CTTCCGCGC	CGCCGCAAGC	GCCTCAGCCA	CCGCGCGCCG	660
GTCCCCGCGC	CCGGGCTGCG	GCCCAGGAG	GCCCCGGGCC	TCCCCGCCG	CCCCGCCGCCC	720
GCGCCCGCCG	CCCCGGCCTC	GCCCCGCATG	CGCTCGCCCG	CCCGCCAGGA	GGAGCGCGCC	780
AGCCCCGCGG	GCAAGTTCTC	CAGCTCCCTC	GCCATCGACA	GCATCTGCG	CAAGCCCTTC	840
CGCAGCCGTC	GCCTCAGGGA	CACGGCCCCC	GGGACGACGC	TTCAGTGGGG	CGCCGCGCC	900
TGCCCGCCGC	TGCCCGCGTT	CCCCGCGCTC	CTCCCCGCGG	CGCCCTGCAG	GGCCCTGCTG	960
CCGCTCTGCG	CGTACGGCGC	GGGCGAGCCG	GCGCGGCTGG	GCGCGCGCGA	GGCCGAGGTG	1020
CCACCGACCG	CGCCGCCCCCT	CCTGCTTGCA	CCTCTCCCGG	CGGCGGCC	CGCCAAGCCA	1080
CTCCGAGGCC	CGGCGGCCGG	CGGCGCGCAC	CTGTACTGCC	CCCTGCGGCT	GCCCCGAGCC	1140
CTGCAGGCCG	CCTTAGTCCG	NCGTCCCTGGC	CCGCACCTGT	CGTACCCGGT	GGAGACGCTC	1200
CTAGCTTGA						

SEQ ID NO:32 Protein sequence:  
Protein Accession #: NP\_150285.1

1	11	21	31	41	51	
MKLEVFPRA	AHGDKQGS	D EGAGGSDAPS	PLSAAGDDSL	GSDGDCAA	KP SAGGGARDTQ	60
GDGEQSAGGG	PGAEAAIPAA	AAA AVVAE	EAGAAAGPGAG	GAGSGEGARS	KPYTRRPKPP	120
YSYIALIAMA	IRDSAGGR	L LT LAEINEYLMG	KFPFFRGSYT	GWRNSVRHNL	SLNDCFVKVL	180
RDPSRPWGKD	NYWMLNPNSE	YTFADGVFR	RRKRLSHRAP	VPAPGLRPEE	APGLPAAPPP	240
APAAPASPRM	RSPARQEERA	SPAGKFSSF	AIDSIILRKPF	RSRRLRDTAP	GTTLQWGAAP	300
CPPLPAFPAL	LPAAPCRALL	PLCAYGAGEP	ARLGAREAEV	PPTAPPLLLA	PLPAAAPAKP	360
LRGPAAGGAH	LYCPLRLPAA	LQAA	LVRRPG	PHLSYPVETL	LA	

SEQ ID NO:33 DNA sequence  
Nucleic Acid Accession #: NM\_012128.2  
Coding sequence: 43-2796

1	11	21	31	41	51	
GAACAAACCA	ACATTGAGC	CAGGAATAAC	TAGAGAGGAA	CAATGGGGTT	ATT CAGAGG	60
TTTGTTC	TCTTAGTTCT	GTGCCTGCTG	CACCAAGTCAA	ATACTTCCTT	CATTAAGCTG	120
AATAATAATG	GCTTGAAGA	TATTGTCATT	GTTATAGATC	CTAGTGTGCC	AGAAGATGAA	180
AAAATAATTG	AACAAATAGA	GGATATGGTG	ACTACAGCTT	CTACGTACCT	GTTTGAAGCC	240
ACAGAAAAAA	GATTTTTTT	CAAAAATGTA	TCTATATTAA	TTCCTGAGAA	TTGGAAGGAA	300
AATCCTCAGT	ACAAAAGGCC	AAAACATGAA	AACCATAAAC	ATGCTGATGT	TATAGTTGCA	360
CCACCTACAC	TCCCAGGTAG	AGATGAACCA	TACACCAAGC	AGTTCACAGA	ATGTGGAGAG	420
AAAGGCGAAT	ACATTCACTT	CACCCCTGAC	CTTCTACTTG	GAAAAAAACAA	AAATGAATAT	480
GGACCACCA	GCAAACGT	TGTCCATGAG	TGGGCTCACC	TCCGGTGGGG	AGTGTGTTGAT	540
GAGTACAATG	AAGATCAGCC	TTTCTACCGT	GCTAAGTC	AAAAAAATCGA	AGCAACAAGG	600
TGTTCCGCA	GTATCTCTGG	TAGAAATAGA	GTTTATAAGT	GTCAAGGAGG	CAGCTGTCTT	660
AGTAGAGCAT	GCAGAATTGA	TTCTACAACA	AAACTGTATG	GAAAAGATTG	TCAATTCTTT	720
CCTGATAAAG	TACAAACAGA	AAAAGCATCC	ATAATGTTA	TGCAAAGTAT	TGATTCTGTT	780
GTTGAATT	GTAACGAAA	AAACCCATAAT	CAAGAAGCTC	CAAGCCTACA	AAACATAAAAG	840
TGCAATT	GAAGTACATG	GGAGGTGATT	AGCAATTCTG	AGGATTAA	AAACACCATA	900
CCCATGGTGA	CACCACCTCC	TCCACCTGTC	TTCTCATTGC	TGAAGATCCG	TCAAAGAATT	960
GTGTGCTTA	TTCTTGATAA	GTCTGGAAGC	ATGGGGGGTA	AGGACCGCCT	AAATCGAATG	1020
AATCAAGCAG	CAAAACATT	CCTGCTGCAG	ACTGTTGAAA	ATGGATCTG	GGTGGGGATG	1080
GTTCACTT	ATAGTACTGC	CACTATTGTA	AATAAGCTAA	TCCAAATAAA	AAGCAGTGAT	1140
GAAAGAAACA	CACTCATGGC	AGGATTACCT	ACATATCCTC	TGGGAGGAAC	TTCCATCTGC	1200
TCTGGAATT	AATATGCATT	TCAGGTGATT	GGAGAGCTAC	ATTCCCAACT	CGATGGATCC	1260
GAAGTACTGC	TGCTGACTGA	TGGGGAGGAT	AACACTGCAA	GTTCTGTAT	TGATGAAGTG	1320
AAACAAAGTG	GGGCCATTGT	TCATTTATT	GCTTGGGAA	GAGCTGCTGA	TGAAGCAGTA	1380
ATAGAGATGA	GCAAGATAAC	AGGAGGAAGT	CATTTTATG	TTTCAGATGA	AGCTCAGAAC	1440

AATGGCCTCA	TTGATGCTTT	TGGGGCTCTT	ACATCAGGAA	ATACTGATCT	CTCCCAGAAG	1500
TCCCTTCAGC	TCGAAAGTAA	GGGATTAAACA	CTGAATAGTA	ATGCCTGGAT	GAACGACACT	1560
GTCATAATTG	ATAGTACAGT	GGGAAAGGAC	ACGTTCTTTC	TCATCACATG	GAACAGTCTG	1620
CCTCCAGTA	TTTCTCTCTG	GGATCCCAGT	GGAACAAATAA	TGGAAAATT	CACAGTGGAT	1680
GCAACTTCCA	AAATGGCCTA	TCTCAGTATT	CCAGGAACGT	CAAAGGTGGG	CACTTGGCA	1740
TACAATCTTC	AAGCCAAAGC	GAACCCAGAA	ACATTAAC	TTACAGTAAC	TTCTCGAGCA	1800
GCAAATTCTT	CTGTGCCTCC	AATCACAGT	AATGCTAAA	TGAATAAGGA	CGTAAACAGT	1860
TTCCCCAGCC	CAATGATTGT	TTACGCAGAA	ATTCTACAAG	GATATGTACC	TGTTCTTGGA	1920
GCCAATGTGA	CTGCTTTCAT	TGAATCACAG	AATGGACATA	CAGAAGTTT	GGAACTTTTG	1980
GATAATGGTG	CAGGCCTGA	TTCTTCAAG	AATGATGGAG	TCTACTCCAG	GTATTTACA	2040
GCATATACAG	AAAATGGCAG	ATATAGCTTA	AAAGTTCGGG	CTCATGGAGG	AGCAAACACT	2100
GCCAGGCTAA	AATTACGGCC	TCCACTGAAT	AGAGCCGCGT	ACATACCAGG	CTGGGTAGTG	2160
AAACGGGAAA	TTGAAGCAA	CCCGCCAAGA	CCTGAAATTG	ATGAGGATAC	TCAGACCACC	2220
TTGGAGGATT	TCAGCCGAAC	AGCATCCGGA	GGTGCATTTG	TGGTATCACA	AGTCCCAAGC	2280
CTTCCCTTGC	CTGACCAATA	CCCACCAAGT	CAAATCACAG	ACCTTGATGC	CACAGTTCAT	2340
GAGGATAAGA	TTATTCTTAC	ATGGACAGCA	CCAGGAGATA	ATTTTGATGT	TGGAAAAGTT	2400
CAACGTTATA	TCATAAGAAT	AAGTGAAGT	ATTCTTGATC	TAAGAGACAG	TTTGATGAT	2460
GCTCTTCAAG	TAAATACTAC	TGATCTGTCA	CCAAAGGAGG	CCAACCTCAA	GGAAAGCTTT	2520
GCATTTAAC	CAGAAAATAT	CTCAGAAGAA	AATGCAACCC	ACATATTAT	TGCCATTAAA	2580
AGTATAGATA	AAAGCAATT	GACATAAAA	GTATCCAACA	TTGCACAAGT	AACTTTGTTT	2640
ATCCCTCAAG	CAAATCCTGA	TGACATTGAT	CCTACTCCTA	CTCCTACTCC	TACTCCTGAT	2700
AAAAGTCATA	ATTCTGGAGT	TAATATTCT	ACGCTGGTAT	TGTCTGTGAT	TGGGTCTGTT	2760
GTAATTGTTA	ACTTTATTTT	AAGTACCACC	ATTGAAACCT	TAACGAAGAA	AAAAATCTTC	2820
AAGTAGACCT	AGAAGAGAGT	TTTAAAAAAC	AAAACAATGT	AAGTAAAGGA	TATTTCTGAA	2880
TCTTAAAATT	CATCCCATGT	GTGATCATAA	ACTCATAAAA	ATAATTAA	GATGTCGGAA	2940
AAGGATACTT	TGATTAATA	AAAACACTCA	TGGATATGTA	AAAACGTCA	AGATTAAAAT	3000
TTAATAGTTT	CATTTATTTG	TTATTTATT	TGTAAGAAAT	AGTGATGAAC	AAAGATCCTT	3060
TTTCATACTG	ATACCTGGTT	GTATATTATT	TGATGCAACA	GTTTCTGAA	ATGATATTTC	3120
AAATTGCATC	AAGAAATTAA	AATCATCTAT	CTGAGTAGTC	AAAATACAAG	TAAAGGAGAG	3180
CAAATAAAC	ACATTGGAA	AAAAAAAAAA	AAAAAAAAAA			

SEQ ID NO:34 Protein sequence:  
Protein Accession #: NP\_036260.1

1	11	21	31	41	51	
MGLFRGFVFL	LVLCLLHQSN	TSFIKLNNG	FEDIVIVIDP	SVPDEDEKII	QIEDMVTTAS	60
TYLFATEKR	FFFKNVSIL	PENWKENPQY	KRPKHENHKH	ADVIVAPPTL	PGRDEPYTKQ	120
FTECGEKGEY	IHFTPDLLL	KKQNEYGPPG	KLFVHEWAHL	RWGVFDEYNE	DQPFYRAKSK	180
KIEATRCGSAG	ISGRNRVYKC	QGGSCLSRA	RIDSTTKLYG	KDCQFFPDKV	QTEKASIMFM	240
QSIDSVVEFC	NEKTHNQEAP	SLQNIKCNFR	STWEVISNSE	DFKNTIPMVT	PPPPPVSLL	300
KIRQRIVCLV	LDKSGSMGGK	DRLNRMNQAA	KHFLLQTVEN	GSWVGVMHFD	STATIVNKLI	360
QIKSSDERNT	LMAGLPTYPL	GGTSICSGIK	YAFQVIGELH	SQLDGSEVLL	LTDGEDNTAS	420
SCIDEVKQSG	AIVHFIALGR	AADEAVIEMS	KITGGSHFYV	SDEAQNNGLI	DAFGALTSGN	480
TDLSQKSQLQ	ESKGTLNSN	AWMNDTVIID	STVGKDFFL	ITWNSLPPSI	SLWDPSGTIM	540
ENFTVDATSK	MAYLSIPGTA	KVGTWAYNLQ	AKANPETLTI	TVTSRAANSS	VPPITVNAKM	600
NKDVNSFPSP	MIVYAEILQG	YVPVLGANVT	AFIESQNGHT	EVLELLDNGA	GADSFKNNDGV	660
YSRYFTAYTE	NGRYSLKVR	HGGANTARLK	LRPPLNRAAY	IPGWWVNGEI	EANPPRPEID	720
EDTQTTLED	SRTASGGAFV	VSQVPSLPLP	DQYPPSQITD	LDA	TVHEDKI	840
FDVGKVQRYI	IRISASIDL	RDSFDDALQV	NTTDLSPKEA	NSKESFAFKP	ENISEENATH	900
IFI	AIKSIDK	SNLTSKVSNI	AQVTLFIPQA	NPDDIDPTPT	PTPTPDKSHN	SGVNISTLVL
SVIGSVVIVN	FILSTTI					

SEQ ID NO:35 DNA sequence

Nucleic Acid Accession #: NM\_000901.1

Coding sequence: 217-3171

1	11	21	31	41	51	
CGCGGGAGCC	AACTTCAGGC	TGCTCAGAGG	AAGCCCGTGC	AGTCAGTCAC	CTGGGTGCAA	60
GAGCGTTGCT	GCCTCGGGCT	CTCCCGCTGC	AGGGAGAGCG	GCACTCGCTG	GCCTGGATGT	120
GGTTGGATT	AGGGGGGCTC	CGCAGCAGGG	GTTTCGTGGC	GGTGGCAAGC	GCTGCAACAG	180
GTAGACGGCG	AGAGACGGAC	CCCAGGCCAG	GCAGGGATGG	AGACCAAAGG	CTACCACAGT	240
CTCCCTGAAG	GTCTAGATAT	GGAAAGACGG	TGGGGTCAAG	TTTCTCAGGC	TGTGGAGCGT	300
TCTTCCCTGG	GACCTACAGA	GAGGACCGAT	GAGAATAACT	ACATGGAGAT	TGTCAACGTA	360
AGCTGTGTT	CCGGTGCTAT	TCCAAACAAC	AGTACTCAAG	GAAGCAGCAA	AGAAAAACAA	420
GAACACTACTC	CTTGCCCTCA	GCAAGACAAT	AATCGGCCTG	GGATTTAAC	ATCTGATATT	480
AAAACGTAGC	TGGAATCTAA	GGAACTTCA	GCAACTGTAG	CTGAGTCCAT	GGGTTTATAT	540
ATGGATTCTG	TAAGAGATGC	TGACTATTCC	TATGAGCAGC	AGAACCAACA	AGGAAGCATG	600
AGTCCAGCTA	AGATTATCA	GAATGTTGAA	CAGCTGGTGA	AATTTACAA	AGGAAATGGC	660
CATCGTCCTT	CCACTCTAAG	TTGTGTGAAC	ACGCCCTTGA	GATCATTAT	GTCTGACTCT	720
GGGAGCTCCG	TGAATGGTGG	CGTCATGCGC	GCCATTGTTA	AAAGCCCTAT	CATGTGTCAT	780
GAGAAAAGCC	CGTCTGTTG	CAGCCCTCTG	AACATGACAT	CTTCGGTTG	CAGCCCTGCT	840
GGAATCAACT	CTGTGTCCTC	CACCACAGCC	AGCTTGGCA	GTTCCTCAGT	GCACAGCCCC	900
ATCACCCAGG	GAACCTCTCT	GACATGCTCC	CCTAATGCTG	AAAATCGAGG	CTCCAGGTGCG	960
CACAGCCCTG	CACATGCTAG	CAATGTGGC	TCTCCTCTCT	CAAGTCCGTT	AAGTAGCATG	1020
AAATCCTCAA	TTTCCAGCCC	TCCAAGTCAC	TGCAGTGTAA	AATCTCCAGT	CTCCAGTCCC	1080
AAATAATGTCA	CTCTGAGATC	CTCTGTGTCT	AGCCCTGCAA	ATATTAACAA	CTCAAGGTGC	1140
TCTGTTTCCA	GCCCTTCGAA	CACTAATAAC	AGATCCACGC	TTTCCAGTCC	GGCAGGCCAGT	1200
ACTGTGGGAT	CTATCTGTAG	CCCTGTAAAC	AATGCCTTCA	GCTACACTGC	TTCTGGCACC	1260
TCTGCTGGAT	CCAGTACATT	GGGGGATGTG	GTTTCCCAGTC	CAGACACGCA	GGAGAAAGGT	1320
GCTCAAGAGG	TCCCTTTTCC	TAAGACTGAG	GAAGTAGAGA	GTGCCATCTC	AAATGGTGTG	1380
ACTGGCCAGC	TTAATATTGT	CCAGTACATA	AAACCAGAAC	CAGATGGAGC	TTTTAGCAGC	1440
TCATGTCTAG	GAGGAAATAG	CAAATAAAAT	TCGGATTCTT	CATTCTCAGT	ACCAATAAAAG	1500
CAAGAATCAA	CCAAGCATT	ATGTTCAAGG	ACCTCTTTA	AAGGGATCC	AACAGTAAAC	1560
CCGTTTCCAT	TTATGGATGG	CTCGTATTT	TCCTTTATGG	ATGATAAAGA	CTATTATTCC	1620
CTATCAGGAA	TTTTAGGACC	ACCTGTGCC	GGCTTTGATG	GTAACTGTGA	AGGCAGCGGA	1680
TTCCCAGTGG	GTATTAAACA	AGAACCCAGAT	GACGGGAGCT	ATTACCCAGA	GGCCAGCCTC	1740
CCTTCCTCTG	CTATTGTTGG	GGTGAATTCA	GGTGGACAGT	CCTTCCACTA	CAGGATTGGT	1800
GCTCAAGGT	CAATATCTT	ATCACGATCG	GCTAGAGACC	AATCTTCCA	ACACCTGAGT	1860
TCCTTCCTC	CTGTCAATAC	TTTAGTGGAG	TCATGGAAAT	CACACGGCGA	CCTGTCGTCT	1920
AGAAGAAGTG	ATGGGTATCC	GGTCTTAGAA	TACATTCCAG	AAAATGTATC	AAGCTCTACT	1980
TTACGAAGTG	TTTCTACTGG	ATCTTCAAGA	CCTTCAAAA	TATGTTGGT	GTGTGGGGAT	2040
GAGGCTTCAG	GATGCCATTA	TGGGGTAGTC	ACCTGTGGCA	GCTGCAAAGT	TTTCTTCAA	2100
AGAGCAGTGG	AAGGGCAACA	CAACTATTTA	TGTGCTGGAA	GAAATGATTG	CATCATTGAT	2160
AAGATTGAC	GAAAGAATTG	TCCTGCTTC	AGACCTCAGA	AATGTCTTC	AGCTGGAATG	2220
AATTAGGAG	CACGAAAGTC	AAAGAAGTTG	GGAAAGTTAA	AAGGGATTCA	CGAGGGAGCAG	2280
CCACAGCAGC	AGCAGCCCCC	ACCCCCACCC	CCACCCCCCGC	AAAGCCCCAGA	GGAGGGGACA	2340
ACGTACATCG	CTCCTGCAA	AGAACCCCTCG	GTCAACACAG	CACTGGTCC	TCAGCTCTCC	2400
ACAATCTCAC	GAGCGCTCAC	ACCTCCCCC	GTTATGGTCC	TTGAAAACAT	TGAACCTGAA	2460
ATTGTATATG	CAGGCTATGA	CAGCTAAAAA	CCAGATACAG	CCGAAAATCT	GCTCTCCACG	2520
CTCAACCGCT	TAGCAGGCAA	ACAGATGATC	CAAGTCGTGA	AGTGGGCAA	GGTACTTCCA	2580
GGATTTAAA	ACTTGCCCT	TGAGGACAA	ATTACCCCTAA	TCCAGTATTC	TTGGATGTGT	2640
CTATCATCAT	TTGCCCTGAG	CTGGAGATCG	TACAAACATA	CGAACAGCCA	ATTTCCTCTAT	2700
TTTGACCCAG	ACCTAGTCTT	TAATGAAGAG	AAGATGCATC	AGTCTGCCAT	GTATGAACTA	2760
TGCCAGGGGA	TGCACCAAAT	CAGCCTTCAG	TTCGTTCGAC	TGCACTCAC	CTTGTGAGAA	2820
TACACCATCA	TGAAAGTTT	GCTGCTACTA	AGCACAATTC	CAAAGGATGG	CCTCAAAAGC	2880
CAGGCTGCAT	TTGAAGAAAT	GAGGACAAAT	TACATCAAAG	AACTGAGGAA	GATGGTAACT	2940
AAGTGTCCC	ACAATTCTGG	GCAGAGCTGG	CAGAGGTTCT	ACCAACTGAC	CAAGCTGCTG	3000
GACTCCATGC	ATGACCTGGT	GAGCGACCTG	CTGGAATTCT	GCTTCTACAC	CTTCCGAGAG	3060
TCCCATGCGC	TGAAGGTAGA	GTTCGGCGCA	ATGCTGGTGG	AGATCATCAG	CGACCAGCTG	3120
CCCAAGGTGG	AGTCGGGGAA	CGCCAAGCCG	CTCTACTTCC	ACCGGAAGTG	ACTGCCCGCT	3180
GCCCAGAAGA	ACTTGCCTT	AAGTTCCCT	GTGTTGTTCC	ACACCCAGAA	GGACCCAAGA	3240
AAACCTGTT	TTAACATGTG	ATGGTTGATT	CACACTTGTT	CAACAGTTTC	TCAAGTTAA	3300

AGTCATGTCA	GAGGTTGGAA	GCCGGGAAAG	CTGTTTTCC	GTGGATTG	CGAGACCA	3360	
GCAGTCTGAA	GGATCCCCA	CCTCCAATCC	CCCAGCGCTT	AGAACATGT	TCCTGTTCT	3420	
CGGGATGAAA	AGCCATATCT	AGTCATAAC	TCTGATTTG	ATATTTCA	AGATGGAAGA	3480	
AGTTTTAACT	ATGCCGTGTA	GTTTCTGGTA	TCGTTCGCTT	GT	TTAAAAGG	3540	
CTAACGAAACG	TTTAAAGCT	TACCCTTGGT	TTGCACATAA	AACGTATAGT	CAATATGGG	3600	
CATTAATATT	CTTTGTTAT	TAAAAAACAA	CAAAAAATA	ATAAAAAAAT	ATATACAGAT	3660	
TCCTGTTGTG	TAATAACAGA	ACTCGTGGCG	TGGGGCAGCA	GCTGCCTCTG	AGCCCTCGCT	3720	
CGTCCACGGT	CTTCTGCATC	ACTGGTATAC	ACACTCGTTA	GCGTCCATT	CTTATTTAAT	3780	
TAGAATGGAT	AAGATGATGT	TAAATGCCTT	GGTTTGATT	CTAGTATCTA	TTGTGTTGGC	3840	
TTTACAATAA	ATTTTTGCA	GTCTTTGCT	GTGCTGTACA	TTACTGTATG	TATAAATTAT	3900	
GAAGGACCTG	AAATAAGGTA	TAAGGATCTT	TTGTAAATGA	GACACATACA	AAAAAAATCT	3960	
TTAATGGTTA	ATAGGATGAA	TGGGAAAGTA	TTTTGAAAG	AATTCTATT	TGCTGGAGAC	4020	
TATTTAAGTA	CTATCTTGT	CTAACACAAGG	TAATTTTTT	TTGTAAAGT	CAATGTCCTG	4080	
CATGCATAAT	GAACCGTTA	CAGTGTATTT	AAGAAAGGGA	AAGCTGTGCC	TTTTTAGCT	4140	
TCATATCTAA	TTTACCATTA	TTTACAGTC	TCTGTTGTAA	ATAACCACAC	TGAAACCTCT	4200	
TCGGTTGTCT	TGAAACCTTT	CTACTTTTC	TGTACTTTT	GT	TTGTTCTCT	4260	
CTTGGGGCAT	TTGTGGGACT	CCAGCACGTT	TTCTGGCTTC	TGCTTCATCC	TGCTCCATCG	4320	
GGGAATGACA	CACTCGGTG	TCTGCAGCTC	CTGGAAGGTG	TCATTGACA	ACACATGTGG	4380	
GAGAGGAGGT	CCTTGGAGTG	CTGCAGCTT	GGGAAAGCCT	GCCTCGTTTC	CCTTTTCCTC	4440	
TAGAAGCAGA	ACCAGCTCTA	CGAGAGTGTG	ACTGGGAACT	TGATGGCTCA	GAGAGCATCT	4500	
TTTCCTCCCA	TTTTAGAAAA	TCAGATTTC	TCCTGTGGGA	AAAAAAATT	CCATGCACTC	4560	
TCTCTCTGTT	AAAGATCAGC	TATTCCCTTC	TGATCTTGG	AAGAGGTTCT	GCAC	CTCCTGG	4620
AACCGGTAC	AGGAACGCAC	AGATCATGGC	AGGATGCGCT	GGGACGGCCC	ATCTTGGCAA	4680	
GGTCAGTCT	GAATGGCATG	GAGACCGGG	GATAGAGGGG	TTTTAGATT	TTAAAAGGTA	4740	
GGTTTTAAAAA	ATAAGTTTA	TACATAAAAC	GT	TTGGAGA	AAAATTACAG	ATCATATAAG	4800
CAAGACAGTG	GCAC	TTAAATTCA	TTAATCTGTT	TGTTTGGCAC	TGATGCAATG	4860	
TATGGCTTTT	CTCTGCCCC	AAATCACAAA	CATATGTATC	TTTGGGAAA	CTAACAAATAT	4920	
GATTGCACTA	AATAAACTAC	TTTGAATAGA	GGCCAAATT	ATCTTTAAA	AATGATGATA	4980	
ATCATCAGGT	TTACTCAGTG	AAATCATATT	AATTATTTT	CAAAATCTAA	AAGCTGTAGC	5040	
TGGAGAAGCC	CATGCCACG	AGGAAGCAGC	AATTAATTAG	ATCAACACTT	TTCTCCAGGG	5100	
TTCACCATGC	AGGCAACATT	ACCTGCTT	TCAAAAGACA	CCTGCCTTAG	TGCAAGGGGA	5160	
AACCTGTGAA	AGCTGCACTC	AGAGGGAGGA	GTCTTCTTA	CATAATTGC	AATTCAGGA	5220	
ATTTAATT	TAGGCAGATC	TTTAAATACA	GTCAACTTAC	GGTGCACAGT	AATATGAAAG	5280	
CCACACTTG	AAGGTAAATAA	ATACACAGCA	TGCA	AGACTGG	GAGTTGCTAG	5340	
GCTTACTTAC	AAAAGCAGCT	TTTAGTTCA	ACTTAGTTT	TATAAAATGA	GAATTCTGAC	5400	
TTACTTAACC	AGGTTGGGA	TGGAGATGGT	CTGCATCAGC	TTTTGTATT	AA	CAAAGTTA	5460
CTGGCTCTT	GTGTGCTCC	AGGTAAC	TT	GCTGATTAA	ACAGCAAAGC	CATATTCTAA	5520
ATTCACTGTT	GAATGCCTGT	CCCAGTCCAA	ATTGCTGTC	TGCTCTTATT	TTTGTACCAT	5580	
ATTGCTCTTA	AAAATCTTGG	TTTGGTACAG	TTCATAATT	ACCAAAAGT	TCATATAATT	5640	
TAAGAACA	CTAAATTAGT	TTAAATGAA	GCAATTATA	TCTTATGCA	AAAACATATG	5700	
TCTGTCTTG	CAAAGGACTG	TAAGCAGATT	ACAATAAATC	CTTTACTTT			

SEQ ID NO:36 Protein sequence:  
Protein Accession #: NP\_000892.1

1	11	21	31	41	51	
METKGYHSLP	EGLDMERRWG	QVSQAVERSS	LGPTERTDEN	NYMEIVNVSC	VSGAIPNNST	60
QGSSKEKQEL	LPCLQQDNNR	PGILTSIDI	KT ELESKELSAT	VAESMGLYMD	SVRDADYSYE	120
QQNQQGSMSP	AKIYQNVEQL	VKFYKGNGHR	PSTLSCVNTP	LRSFMSDSGS	SVNGGVMR	180
VKSPIIMCHEK	SPSVCSPLN	TSSVCSPAGI	NSVSSTTASF	GSFPVHSPIT	QGTPLTCS	240
AENRGSRSHS	PAHASNVGSP	LSSPLSSMKS	SISSPPSHCS	VKSPVSSPNN	VTLRSSVSSP	300
ANINNSRC	SSPSNTNNR	TLSSPAASTV	GSICSPVNNA	FSYTASGTSA	GSSTLRDVVP	360
SPDTQEKGAAQ	EVPFPKTEEV	ESAISNGVTG	QLNIVQYIKP	EPDGAFSSSC	LGGNSKINS	420
SSFSVPPIKQ	STKHSCSGTS	FKGNPTVNP	PFMDGSYFSF	MDDKDYYSL	GILGPPVPGF	480
DGNCEGSGFP	VGIKQEPDDG	SYYPEASIPS	SAIVGVNSGG	QSFHYRIGAQ	GTISLSRSAR	540
DQSFQHLSSF	PPVNTLVESW	KSHGDLSSRR	SDGYPVLEYI	PENVSSSTLR	SVSTGSSRPS	600
KICLVC	SGCHYGVVTC	GSCKVFFKRA	VEQHNYLCA	GRND	CIIDKI RRKNCPACRL	660
QKCLQAGMNL	GARKSKKL	GK LKG IHEEQPQ	QQQQPPPPPPP	PQSPEEGTT	IAPAKEPSVN	720
TALVPQLSTI	SRALTPSPVM	VLENIEPEIV	YAGYDSSKPD	TAENLLSTLN	RLAGKQMIQV	780

VKWAKVLPGF	KNLPLEDQIT	LIQYSWMCLS	SFALSWRSYK	HTNSQFLYFA	PDLVFNEEKM	840
HQSAMYELCQ	GMHQISLQFV	RLQLTSEEYT	IMKVLLLLST	IPKDGLKSQA	AFFEEMRTNYI	900
KELRKMVTKC	PNNSGQSWQR	FYQLTKLLDS	MHDLVSDLLE	FCFYTFRESH	ALKVEFPAML	960
VEIIISDQLPK	VESGNAKPLY	FHRK				

SEQ ID NO:37 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
CCTACCAGGT	TCAAGCAACT	CTGCTGCCTC	AGCTCCCAAG	TAGCTGGGAT	TACAGGTGCA	60
TGCCACTACA	CCTGGCTTTT	TGTATTTTA	GTAGAGATGG	TTTTCACTAT	GTTGGCCAGG	120
CTGATCTTGA	ATTCCTGGCC	TGAAGTAATC	TGCCTGCCTC	AGCCTCCAA	AGTGTGGGA	180
TTATAGGAGC	CACCACACCT	GGCATAACTG	GTATTTTTA	TATGCTTCCT	GGGCAACTTA	240
AAAAATTGAT	TACTCTGTTG	TTTCTTCCTT	TTTTTTTTT	TTTTGGCTTT	GACCAATTG	300
TGAGACCCAA	GTATCTCCTA	CCTAGAAAAA	AAACACACTA	AACAGTAAAT	GATTACCAAC	360
CTATTTGGAA	CAAATCTCAA	TTAATTAACA	TATACCTCAA	GGAGAAGACT	TAACAAAATC	420
TTACTTTCA	TTCTTAATAG	CTCTTCCAT	AAAAATGTTC	CACAAGTGT	TCAAATTAGT	480
CCTAACAACT	ACTGTTAAGT	GATTAATGAA	ACAGGAGTGA	CAGGAGTGA	TTTAATAATA	540
GCAATAAATA	CAGATGGGAC	TACATAAATT	GTGGAGGTCC	TGATGCAAAA	CTCTCTCTGT	600
ATTCGATGGC	ATCTCAGCTT	TCTCATAGAG	CTGTTCACT	GTGAGGGTCT	TTATCCTTC	660
TGCAGAGCTT	CATTATTTTC	TTTCTTCAG	CAATCAGTCC	AAAGCACAAT	GTCAGAAAGA	720
TCACAACACA	TGCAGCAATA	ATGGGCTCTA	TTGGTACACC	CACAGTTTA	TCTTTAACAA	780
TC						

SEQ ID NO:38 DNA sequence

Nucleic Acid Accession #: NM\_001192.1

Coding sequence: 219-773

1	11	21	31	41	51	
AAGACTCAAA	CTTAGAAACT	TGAATTAGAT	GTGGTATTCA	AATCCTTACG	TGCCCGGAAG	60
ACACAGACAG	CCCCCGTAAG	AACCCACGAA	GCAGGCGAAG	TTCATTGTT	TCAACATTCT	120
AGCTGCTCTT	GCTGCATTG	CTCTGGAATT	CTTGTTAGAGA	TATTACTTGT	CCTTCCAGGC	180
TGTTCTTCT	GTAGCTCCCT	TGTTTCTTT	TTGTGATCAT	GTTGCAGATG	GCTGGGCAGT	240
GCTCCCAAAA	TGAATATTTT	GACAGTTGT	TGCATGCTTG	CATACCTTGT	CAACTTCGAT	300
GTTCTCTAA	TACTCCTCCT	CTAACATGTC	AGCGTTATTG	TAATGCAAGT	GTGACCAATT	360
CAGTGAAAGG	AACGAATGCG	ATTCTCTGGA	CCTGTTGGG	ACTGAGCTTA	ATAATTCTT	420
TGGCAGTTT	CGTGCTAATG	TTTTGCTAA	GGAGAGATAAG	CTCTGAACCA	TTAAAGGACG	480
AGTTTAAAAA	CACAGGATCA	GGTCTCCTGG	GCATGGCTAA	CATTGACCTG	GAAAAGAGCA	540
GGACTGGTGA	TGAAATTATT	CTTCCGAGAG	GCCTCGAGTA	CACGGTGGAA	GAATGACCT	600
GTGAAGACTG	CATCAAGAGC	AAACCGAAGG	TGCACTCTGA	CCATTGCTTT	CCACTCCCAG	660
CTATGGAGGA	AGGCCAAC	ATTCTTGTC	CCACGAAAAC	GAATGACTAT	TGCAAGAGCC	720
TGCCAGCTGC	TTTGAGTGCT	ACGGAGATAG	AGAAATCAAT	TTCTGCTAGG	TAATTAACCA	780
TTTCGACTCG	AGCAGTGCCA	CTTTAAAAAT	CTTTGTCAG	AATAGATGAT	GTGTCAGATC	840
TCTTTAGGAT	GACTGTATT	TTCAGTTGCC	GATACAGCTT	TTTGTCCCT	AACTGTGGAA	900
ACTCTTATG	TTAGATATAT	TTCTCTAGGT	TACTGTTGGG	AGCTTAATGG	TAGAAACTTC	960
CTTGGTTCA	TGATTAAGT	CTTTTTTTT	CCTGA			

SEQ ID NO:39 Protein sequence:

Protein Accession #: NP\_001183.1

1	11	21	31	41	51	
MLQMAGQCSQ	NEYFDPLLHA	CIPCQLRCSS	NTPPLTCQRY	CNASVTNSVK	GTNAILWTCL	60
GLSLIISLAV	FVLMFLLRKI	SSEPLKDEFK	NTGSGLLGMA	NIDLEKSRTG	DEIILPRGLE	120
YTVEECTCED	CIKSKPKVDS	DHCFPLPAME	EGATILVTTK	TNDYCKSLPA	ALSATEIEKS	180
ISAR						

SEQ ID NO:40 DNA sequence

Nucleic Acid Accession #: NM\_025087.1

Coding sequence: 183-2282

1	11	21	31	41	51	
ACACTGCCTC	GGTCGGCAA	GTGGGTCAGT	TGGCTGGGGC	TCACTTGGCA	ACGGGACGCG	60
GGAACGAGGG	GCGCGGACGC	AGGCCCGGGA	GGACGCGGCG	GCGGGAACCT	GGGGGCGCAG	120
GGCTAGGGCA	GCGGGCCCGA	CCCGCACCGC	TTTCTGGAA	AGCGCTGCC	CTCGCCGCGG	180
CGATGACCTC	GCTGTGGAGA	GAAATCCTCT	TGGAGTCGCT	GCTGGGATGT	TTTCTTGGT	240
CTCTCTACCA	TGACCTGGGA	CCGATGATCT	ATTACTTTCC	TTTGCAAACA	CTAGAACTCA	300
CTGGGCTTGA	AGGTTTTAGT	ATAGCATTC	TTTCTCCAAT	ATTCCCTAAC	ATTACTCCTT	360
TCTGGAAATT	GGTTAACAAAG	AAGTGGATGC	TAACCCCTGCT	GAGGATAATC	ACTATTGGCA	420
GCATAGCCTC	CTTCCAGGCT	CCAAATGCCA	AACTTCGACT	GATGGTTCTT	GCGCTTGGGG	480
TGTCTTCCTC	ACTGATAGTG	CAAGCTGTGA	CTTGGTGGTC	AGGAAGTCAT	TTGCAAAGGT	540
ACCTCAGAAT	TTGGGGATTC	ATTTAGGAC	AGATTGTTCT	TGTTGTTCTA	CGCATATGGT	600
ATACTTCACT	AAACCCAATC	TGGAGTTATC	AGATGTCCAA	CAAAGTGATA	CTGACATTAA	660
GTGCCATAGC	CACACTTGAT	CGTATTGGCA	CAGATGGTGA	CTGCAGTAAA	CCTGAAGAAA	720
AGAAGACTGG	TGAGGTTAGCC	ACGGGGATGG	CCTCTAGACC	CAACTGGCTG	CTGGCAGGGG	780
CTGCTTTGG	TAGCCTTGTG	TTCTCACCC	ACTGGGTTT	TGGAGAAGTC	TCTCTTGT	840
CCAGATGGGC	AGTGAGTGGG	CATCCACATC	CAGGGCCAGA	TCCTAACCCA	TTGGAGGTG	900
CAGTACTGCT	GTGCTTGGCA	AGTGGATTGA	TGCTTCCATC	TTGTTTGTGG	TTTCGTGGTA	960
CTGGTTTGAT	CTGGTGGGTT	ACAGGAACAG	CTTCAGCTGC	GGGGCTCCTT	TACCTGCACA	1020
CATGGGCAGC	TGCTGTGTCT	GGCTGTGTCT	TCGCCATCTT	TACTGCATCC	ATGTGGCCCC	1080
AAACACTTGG	ACACCTTATT	AACTCAGGGA	CAAACCTGG	GAAAACCATG	ACCATTGCCA	1140
TGATATTTA	TCTCTAGAA	ATATTTTCT	GTGCCTGGTG	CACAGCTTTT	AAGTTTGTCC	1200
CAGGAGGTGT	CTACGCTAGA	GAAAGATCAG	ATGTGCTTTT	GGGGACAATG	ATGTTAATTA	1260
TCGGGCTGAA	TATGCTATT	GGTCCTAAGA	AAAACCTTG	TTTGCTTCTT	CAAACAAAAAA	1320
ACAGTTCTAA	AGTGCTTTTC	AGAAAGAGTG	AAAAATACAT	GAAACTTTT	CTGTGGCTGC	1380
TTGTTGGTGT	GGGATTGTTG	GGATTAGGAC	TACGGCATAA	AGCCTATGAG	AGAAAACATGG	1440
GCAAAGTGGC	ACCAACAAA	GAGGTCTCTG	CTGCCATCTG	GCCTTCAGG	TTTGGATATG	1500
ACAATGAAGG	GTGGTCTAGT	CTAGAAAGAT	CAGCTCACCT	GCTCAATGAA	ACAGGTGCAG	1560
ATTCATAAAC	AATTTGGAG	AGTGATGCTT	CTAACCCCTA	TATGGGAAC	AATGACTTAA	1620
CCATGTGGCT	AGGGAAAAG	TTGGGTTCT	ATACAGACTT	TGGTCCAAGC	ACAAGGTATC	1680
ACACTGGGG	GATTATGGCT	TTGTCAAGAT	ACCCAATTGT	GAAATCTGAG	CATCACCTTC	1740
TTCCGTCACC	AGAGGGCGAG	ATCGCACCG	CCATCACATT	GACCGTTAAC	ATTTCGGGCA	1800
AGCTGGTGG	TTTGTCTGT	ACACACTTG	GGAACACAGA	AGATGACCTC	GACAGGAAAC	1860
TGCAGGCTAT	TGCTGTTCA	AAACTACTGA	AAAGTAGCTC	TAATCAAGTG	ATATTTCTGG	1920
GATATATCAC	TTCAGCACCT	GGCTCCAGAG	ATTATCTACA	GCTCACTGAA	CATGGCAATG	1980
TGAAGGATAT	CGACAGCACT	GATCATGACA	GATGGTGTGA	ATACATTATG	TATCGAGGGC	2040
TGATCAGGTT	GGGTTATGCA	AGAATCTCCC	ATGCTGA	GAGTGATTCA	GAAATTCAAGA	2100
TGGAAAATT	TAGGATCCCT	GATGACCCCA	CTAATTATAG	AGACAACCA	AAAGTGGTCA	2160
TAGACCACAG	AGAAGTTCT	GAGAAAATTC	ATTAAATCC	CAGATTGGA	TCCTACAAAG	2220
AAGGACACAA	TTATGAAAAC	AACCATAATT	TTCATATGAA	TACTCCAAA	TACTTTTAT	2280
GAAACATT	AAACAAGAAG	TTATTGGCTG	GGAAAATCTA	AGAAAAAAAG	TATGTAAGAT	2340
AAAAAGAAGA	GATTAATGAA	AGTGGGAAAAA	TACACATGAA	GAACCTCAAC	TTAAAAAACAA	2400
CATGGTATCT	ATGCAGTGGG	AAATTACCTC	CATTGTAAA	CTATGTTGCT	TAATAAAAAC	2460
ATTCCTCTAA	AAAAAAA	AAAAAA				

SEQ ID NO:41 Protein sequence:

Protein Accession #: NP\_079363.1

1	11	21	31	41	51	
MTSLWREILL	ESLLGCVSWS	LYHDLGPMIY	YFPLQTLLELT	GLEGFSIAFL	SPIFLTITPF	60
WKLVKKWML	TLLRIITIGS	IASFQAPNAK	LRLMVLALGV	SSSLIVQAVT	WWSGSHLQRY	120
LRIWGFILGQ	IVLVVLRIWY	TSLNPIWSYQ	MSNKVILTLS	AIATLDRIGHT	DGDCSKPEEK	180
KTGEVATGMA	SRPNWLLAGA	AFGSLVFLTH	WVFGEVSLVS	RWAVSGHPHP	GPDPNPFGGA	240
VLLCLASGLM	LPSCLWFRGT	GLIWWVTGTA	SAAGLLYLHT	WAAAASVSGCVF	AIFTASMWPQ	300
TLGHLINSGT	NPGKTMIA	IFYLLEIFFC	AWCTAFKFVP	GGVYARERSD	VLLGTMMI	360

GLNMLFGPKK NLDLLLQTKN SSKVLFRKSE KYMKLFLWLL VGVGLLGLGL RHKAYERKLG	420
KVAPTKEVSA AIWPFRFGYD NEGSSLERS AHLLNETGAD FITILESDAS KPYMGNNDLT	480
MWLGEKLGFY TDFGPSTRYH TWGIMALSRY PIVKSEHHLL PSPEGEIAPA ITLTVNISGK	540
LVDFVVTHFG NHEDDLDRKL QAIAVSKLLK SSSNQVIFLG YITSAPGSRD YLQLTEHGNV	600
KDIDSTDHDR WCEYIMYRGL IRLGYARISH AELSDSEIQM AKFRIPDDPT NYRDNQKVVI	660
DHREVSEKIH FNPRFGSYKE GHNYENNHF HMNTPKYFL	

**TABLE 25:**

**Table 25** depicts SEQ ID NO: Seq ID No., UnigeneID, UnigeneTitle, Pkey, and ExAccn for all of the sequences in Table 26. SEQ ID NO: Seq ID No links the nucleic acid and protein sequence information in Table 26 to Table 25.

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
SEQ ID NO: Seq ID No.	SEQ ID NO: Sequence Identification Number found in Table 26			
Pkey	ExAccn	UnigeneID	Unigene Title	<u>SEQ ID NO: Seq ID No.</u>
426101	AL049987	Homo sapiens mRNA; cDNA DKFZp564F112 (fr gb	Homo sapiens mRNA; cDNA DKFZp564F112 (fr gb	1-5 4-4 6 & 7 5-6
419145	N99638	DKFZp434A0131 protein		8 & 9 7-8
426818	AA554827	Hs.340046	Homo sapiens cDNA	10 9
421057	T58283		secreted phosphoprotein 1 (osteopontin,	11 & 12 10-11
			cadherin 3, type 1, P-cadherin (placenta	13 & 14 12-13
409041	AB033025	Hs.50081	Hypothetical protein, XP_051860 (KIAA119	15 & 16 14-15
443162	T49951	Hs.9029	DKFZP434G032 protein	17 & 18 16-17
436385	BE551618	Hs.144097	ESTs	19-21 18-20
447033	AI357412	Hs.157601	ESTs	22 & 23 21-22
439608	AW864696	Hs.301732	hypothetical protein MGC5306	24-28 23-27
449032	AA045573	Hs.22900	nuclear factor (erythroid-derived 2)-lik	29 & 30 28-29
442577	AA292998	Hs.163900	ESTs	31 & 32 30-34
429970	AK000072	Hs.227059	chloride channel, calcium activated, fam	33 & 34 32-33
424566	M16801	Hs.1790	nuclear receptor subfamily 3, group C, m	35 & 36 34-35
457407	AA505035	Hs.345911	ESTs	37 36
430378	Z29572	Hs.2556	tumor necrosis factor receptor superfamily	38 & 39 37-38
417332	AW972717	Hs.288462	hypothetical protein FLJ21511	40 & 41 39-40

**Table 26**

SEQ\_ID\_NO:1 Seq\_ID\_No:1 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
CAATATACTGTA	CAATAACTAT	TTGCATGACA	TTTACATCGG	ATATTATGAG	TGATCTAGAG	60
TTGATATGAA	GTATATGGGA	GGATGTGCAA	AGGTGATGTG	CAAATACTAT	GTCATTTAT	120
AGGGGGGACT	TGAGTATCCT	TTGTTACCT	CAGGAGATCC	TGAAACCAGT	CCCCCATGGA	180
TACTGAGGGC	TGACTGTATA	GTCCTATCCT	CACGGAACTT	TCATTCTAAT	GGGGGAAGAC	240
TGACTATAAA	CAAAATATAT	GTAATAGGTG	GTGTTAAGTA	CCGTGGAGAA	GTAACAAATG	300
GGGCAAAGTG	AGTTATACAG	CTCCATTCTT	AGAAACCTTG	GAGTACTTTT	CTTAGTTTAT	360
ACTCGTGGTG	GTTTCCTTT	GTCTCCTTA	TTACATGGGA	CTCTGACATG	TGCCCATAGC	420
TAGGGTGACA	GTAGGATCTA	CCCGATAGTA	GGGTGGCAGT	AGGATCTACC	AAAAAAGCGT	480
CCTGCTGATA	CAGGACAAA	GCATCCTGTT	GTTCCTCGAGC	CTATAAAAAG	AGCTAATGGT	540
GTTGCTTCTC	TTAACATGTGG	CCTCCTACAC	TGTGTTTGG	ATGATTGGTG	ATGTCTTGGA	600
TATTCTGTT	CTTTGGAACT	TTGAATATAC	AACACTTTAC	TAGGGAAATTA	GCAATGGAAG	660
CAGAGCAAAG	ATGTACAGAG	GAAACAATGC	GTAACTCTGA	TGGAATTGAA	GTCATGAGGC	720
AGCAGAGAGC	TTAAATTACA	GCTTTAAAAA	TTTTTATTTT	TTAGAGGGAA	TTTACTTGGG	780
AGTAACAGCA	GTAATAGTTA	ACGGAGCCAG	AATGCTTGAG	TCATATAATT	GCAAAGCAGA	840
GTTGGGAGCA	ACAGATGCTA	AAGAGTAGTT	GCTGTAGTTC	CTCTTTGGGT	CGTAGGAGCA	900
GTTGTCATAT	TACTATATAG	CTACTGCATG	AAGAAGAGTT	CTTAGTGAGG	CCTGGGTGAA	960
CAGCTCTCT	TAGTATTCTG	TGTGACCCCA	TTTGACCTTT	TAACAAATCC	CTAAGTAAAT	1020
AAATAGCCCC	TCAGGAAAAC	TAAGTTTTTC	TCTGCTGTTT	TTTTGCTTGA	GAGAGCTATA	1080
ACTGTAATAG	ACTTATATT	CTGAACATT	TAGTGCTTGC	CAATATTGG	TAATATTAT	1140
GTTTCCTATA	TTTGTAAATGA	ACATTCTCT	TCCGGTACAT	TTTTTGTAA	ATTATTGTTT	1200
GATGGATAAA	AGTTCACCTT	TTATTGTATA	AAATTGACTG	AGATTAATT	ATACACATTG	1260
ACAATGGGTA	AATAGAATT	TTCAAGATT	AAACAGCTGA	AGGATGACCA	CGTAAGCAAA	1320
AAAAAAAAAA	AAAAAACCAA	CAAAATAAA	CCCAAACCCC	TCAAACATT	TCGAACACGA	1380
ACATTCTTC	TGATGCCGGC	ATCCCTGTT	GCAGGTGTGA	AGGGGCAGG	AATCAGCGAG	1440
GTGTCCTGGG	CTGAGTCCCC	GGGGAAAGAAT	ATGAT			

SEQ\_ID\_NO:2 Seq\_ID\_No:2 DNA sequence

Nucleic Acid Accession #: X83301.1

1	11	21	31	41	51	
GCAAAGCCAG	CTGGGCTCCT	GAGTCCGGTC	GGTACTTGGG	GAACTTACTA	CGTCTAGCTG	60
GAGGATTGTA	AATGCACCAA	TCAGCATGCT	GTGTCTAGCT	CAAGATTTC	TCCATCCCCT	120
TATTGTTGGC	CAGTGGCTGT	CATTACATAT	GAGATGAGTC	TCTTGAAGAC	TACAGATGAA	180
CTCAAGCTCC	ATGAGGAGAT	GTTTCATTGT	CGAGAGCAGT	CATGATGGCC	TGCACTCCAC	240
ACAATGCAAC	AGAGTGAAAG	AGCAGGTTCT	GCTCTTTGG	TGTAGTCCTG	AAGCTTCTA	300
AGAAAATTCA	CATCAGGTGA	TGGATAGGAG	CAACCCGTGA	AAACCAGCCT	TAGACTATT	360
TTCAAACAGG	CTGGTGAATT	ACCAAGATCTC	CGTCAAGTGC	AGTAACCAGT	TCAAGTTGGA	420
AGTGTGTCTT	TTGAATGCAG	AGAACAAAGT	CGTGGACAAAC	CAGGCTGGGA	CCCAGGGCCA	480
GCTGAAGGTG	CTGGGTGCCA	ACCTCTGGTG	GCCGTACCTG	ATGCACGAAC	ACCCCGCCTA	540
CCTGTACTCC	TGGGAGGATG	GTGATTGCTC	ACACCAAAGC	CTTGGACCCC	TCCCAGCCTG	600
TGACCTTTGG	GACCAACTCC	ACCTACGCGAG	CAGACAAGGG	GGCTCTGTAT	GTGGATGTGA	660
TCCGTGTGAA	CAGCTACTAC	TCTTGGTATC	GCAACTACGG	GCACCTGGAG	TTGATTGCGC	720
TGCAGCTGGC	CGCCCAAGTT	GAGAATTGGT	GTGAGACATC	ACAATCCAT	TATTCAAGAGC	780
CGCTATGGAG	TGGAAACGCT	TGTAGGGTTT	CACCAGGGCT	GGTGAATTAC	CAGATCTCCG	840
TCAAGTGCAG	TAACCAGTT	AAGTTGGAAG	TATGTCTTT	GAATGCAGAA	AACAAAGTCG	900
TGGACAACCA	GGCTGGGACC	CAGGGCCAGC	TGAAGGTGCT	GGTGCCAACC	TCTGGTGGCC	960
GTACCTGATG	CACGAACACC	CCGCCTACCT	GTACTCGTGG	GAGGATGGTG	ATTGCTCAC	1020
CCAAAGCCTT	GGACCCCTCC	CAGCCTGTGA	CCTTGGGAC	CAACTCCACC	TACGCAGCAG	1080
ACAAGGGGGC	TCTGTATGTG	GATGTGATCC	GTGTGAACAG	CTACTACTCT	TGGTATCGCA	1140
ACTACGGGCA	CCTGGAGTTG	ATTGGCTGC	AGGCCCTGCA	GCTGGCCGCC	CAGTTTGTGA	1200
ATTGGTGTAA	GACATCACAA	TCCCATTATT	CAGAGCGCGT	ATGGAGTGGGA	AACGCTTGTGA	1260

GGGTTTCACC	AGTCTTCCC	AGGGAACTCC	GATGAAGTGT	TCCAACAAAA	TGAGCGAGTG	1320
AACCAAGAAG	AGGATGACAT	TAGATCCAGG	AGATACAACA	GAGGAGATAA	TCTCCAGGAT	1380
GCCTGTGAAG	AAAGATCCCT	GGATCCCAGG	ATGATTATAG	GACAAGTTGT	TCATAATCCA	1440
GCAGGCCAGA	AGACTTCCAG	GGAAACTCAT	TTCAAGATGA	AAATGGACCA	GCCGCAGTGG	1500
CTCACGCCTG	TAATACCAGC	ACTTTGGGAG	GCTGAGGCAG	GCGGATCACT	TGAGGTCAAG	1560
AGTTTGAAC	TAGCCTGGCC	AACGTGGCAA	AACTCCATCT	CTATTAAGA	TACAAAATT	1620
AGCCAGGCAT	AGTGGTGCAT	GCCTGTAGTC	CCAGCTACTT	GGGATGCTGA	GGCAGGAAGA	1680
ATTGCTTGA	CCTGGGAGGC	AGAGTCTGCG	GTGACCGAGA	TCATGCCACT	GCACTCCAGC	1740
CTGGGTGACA	GAGCCAGACT	CCGTCTCTAC	AAAAAAAAAA	AAAAAAAAAA	AAA	

SEQ ID NO:3 Seq ID NO:3 Protein sequence:

Protein Accession #: CAA58280.1

1	11	21	31	41	51	
MDRSNPVKPA	LDYFSNRLVN	YQISVKCSNQ	FKLEVCLLNA	ENKVVDNQAG	TQQLKVLGA	60
NLWWPYLMHE	HPAYLYSWED	GDCSHQSLGP	LPACDLWDQL	HLRSRQGGSV	CGCDPCEQLL	120
LLVSQRLAPG	VDSAAAGRPV					

SEQ ID NO:4 Seq ID NO:4 DNA sequence

Nucleic Acid Accession #: BC002622.1

1	11	21	31	41	51	
GGCACGAGGC	TCCGCCCCGCG	GCCGGGATGC	ACTAGGAAA	GCCAGCTGGG	CTCCTGAGTC	60
CGGTGGGTAC	TTGGAGAACT	TACTACGTCT	AGCTGGAGGA	TTGTAAATGC	ACCAATCAGC	120
ATGCTGTGTC	TAGCTCAAGA	TTTTCTCCAT	CCCTTATTT	TGGGCCAGTG	GCTGTCATTA	180
CATATGAGAA	CTCAAGCTCC	ATGAGGAGAT	GTTTCATTGT	CGAGAGCAGT	CATGATGGCC	240
TGCACCTCAC	ACAATGCAAC	AGAGTAAAG	AGCAGGTTCT	GCTTCTTGG	TGTAGTCCTG	300
AAGCTTCCTA	AGAAAACATTCA	CATCAGGTGA	TGGATAGGAG	CAACCCTGTA	AAACCAGCCT	360
TAGACTATT	TTCAAAACAGG	CTGGTGAATT	ACCAAGATCTC	CGTCAAGTGC	AGTAACCAGT	420
TCAAGTTGGA	AGTGTGTCTT	TTGAATGCAG	AAAACAAAGT	CGTGGACAAC	CAGGCTGGGA	480
CCCAGGGCCA	GCTGAAGGTG	CTGGGTGCCA	ACCTCTGGTG	GCCGTACCTG	ATGCACGAAC	540
ACCCCGCCTA	CCTGTACTCG	TGGGAGGATG	GTGATTGCTC	ACACCAAAGC	CTTGGACCCC	600
TCCCAGCCTG	TGACCTTTGT	GACCAACTCC	ACCTACGCAG	CAGACAAGGG	GGCTCTGTAT	660
GTGGATGTGA	TCCGTGTGAA	CAGCTACTAC	TCTGGTATC	GCAACTACGG	GCACCTGGAG	720
TTGATTTCAGC	TGCAGCTGGC	CGCCCAGTT	GAGAATTGGT	GTAAGACATC	ACAATCCCAT	780
TATTTCAGAGC	GCGTATGGAG	TGGAAACGCT	TGTAGGGTTT	CACCAGTCTT	TCCCAGGGAA	840
CTCCGATGAA	GTGTTCCAAC	AAAATGAGCG	AGTGAACCAA	GAAGAGGATG	ACATTAGATC	900
CAGGAGATAC	AACAGAGGAG	ATAATCTCCA	GGATGCCCTGT	GAAGAAAGAT	CCCTGGATCC	960
CAGGATGATT	ATAGGACAAG	TTGTTCATAA	TCCAGCAGGC	CAGAAGACTT	CCAGGGAAAC	1020
TCATTCAAGG	AGGTAAAAT	GATGGATGAC	TCCTCCAAGA	TGAAATGGA	CCAGCCGCAG	1080
TGGCTCACGC	CTGTAATACC	AGCACTTTGG	GAGGCTGAGG	CAGCGGGATC	ACTTGAGGTC	1140
AGGAGTTGA	AACTAGCCTG	GCCAACGTGG	CAAAACTCCA	TCTCTATTAA	AAATACAAAA	1200
ATTAGCCAAG	CATAGTGGTG	CATGCCTGTA	GTCCCAGCTA	CTTGGGATGC	TGAGGCAGGA	1260
AGAATTGCTT	GAACCTGGGA	GGCAGAGTCT	ACAGTGAGCC	GAGATCATGC	CACTGCACTC	1320
CAGCCTGGC	AACACAGTGA	GACTCCATCT	AAAAAAAAAA	AAAAAAAAAA	AA	

SEQ ID NO:5 Seq ID NO:5 Protein sequence:

Protein Accession #: AAH02622.1

1	11	21	31	41	51	
MDRSNPVKPA	LDYFSNRLVN	YQISVKCSNQ	FKLEVCLLNA	ENKVVDNQAG	TQQLKVLGA	60
NLWWPYLMHE	HPAYLYSWED	GDCSHQSLGP	LPACDLCDQL	HLRSRQGGSV	CGCDPCEQLL	120
LLVSQRLAPG	VDSAAAGRPV					

SEQ ID NO:6 Seq ID NO:6 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
ACCTGAGATC	AGGAGTTCGA	GATCAGCCTG	ACCAATAGGG	TGAAACCCCG	TCTCTACTAA	60
AAATAACAAAA	AATTAGCTGG	ACACGATGGT	GGGTGCCTGT	GGTCCCAGGCT	ACTCGGGAGG	120
CTGAGACAGG	AGAACATCAGTT	GACCTGGGAG	TTGGTGGTTG	CAGTGAGCTG	AGATCACACC	180
ATTGCATTCC	AAGCCTGGC	AACAAGAGTG	AAACTCCATC	GCAAAAAAAA	AAAAGAAGGG	240
GCATAATTG	TGGATGAGGA	TTGGATATAA	GGTAAAGGAT	GGGACATTCT	TGGACTTACA	300
GATGGTGTGA	TTGCCTGGCT	AGAAGAAGAA	TTCCCGGTCA	AAAAGAAACC	ATCAGCTTTC	360
CAAGTGTGAA	AGAGAGATAA	ATCTGTGAAG	ATTATAGGGA	CTACAGGAAA	CTTAATCTTT	420
TTCTTGAAA	AAGCAATTGT	AGCAAAAAAA	AAGAAAATT	CTTACTGTCA	TCTAAAATTG	480
ACATGGACAT	CTTAGTGGAC	TAGAAGTAA	GGGCATAAAAT	TCTCCCAGTG	ATTTTTAATT	540
TTAGCATTGT	GATTAACACC	TTCTAAAATT	GCCAGAACTT	AATAAAATAAT	TGCTTTTCAT	600
TATTAGTATG	CCATCAAATT	TAGTAGCTGT	TTCAAGGCTTT	AATGTGTCAA	GCCTAAAATC	660
CAGATTTTG	AGGATCTCT	CCCTCTTAAA	AGAGTATTCA	GTAACTGCC	GTAGAAATAC	720
ACATGTATAC	AAGGGCACTG	TATACATCAG	TCTAAAAAAT	AAAATATGT	ATACGTTCTG	780
GTGAGTCTAG	CACAGCATTG	CCCAATAGAA	ATACCAATGG	AGTCACAAA	TGTGGCCCAT	840
ATAGGTTAAT	TGGTAAATT	TCTNATAGNC	ACC			

SEQ ID NO:7 Seq ID NO:7 DNA sequence

Nucleic Acid Accession #: AK000942

Coding sequence: 1204-1503

1	11	21	31	41	51	
GTAAAGGAAT	GTCTTTTAA	TTCAGCTTT	CTTTTCTCCA	TGCTAGTGT	ATCAGGTTTT	60
GGTATTATT	TACTTACAGC	ATATGTTATG	AAGCTGGTTT	GAAAATTGGT	TTTAGATATA	120
TCTGCAAGTT	TACTACTTTG	ACTGTAAAAA	AAAAAAATGA	AAAAGTAGTT	GACATCTGTC	180
CTCAGAAGAA	GTTTGCAGGT	TGCATATTG	TGTGAAATA	CACAGGCTAA	AAGGTAATT	240
ATGTTCTTG	GBAATTGAAA	TGGTCAGTGG	CCCGTTACAG	AAACTTATCA	GTCATATATC	300
AGCACCAGTT	CATTCTTTG	CACCTTAGGG	ACCATCTGTC	CCCTGAGGTG	ACCTGAGAAA	360
CAACCAGTTG	CCCACAGACT	GTTATTTCTT	CAAGTGAGCC	AGGATTGAT	TTCACTGCCT	420
TATATTCTAT	TTTTAGTGT	CAGTGCTTG	ATTTTTGGA	AAAACTAAAT	TTTAAACATA	480
TTGAAAAAAT	GTTATAAGAC	TTGGACATTA	AGTCTGTTGA	TAGCCAAAGT	CAGTTTACCA	540
AAGTAAAACA	AATAAATTCT	ATGCTTCTTC	ATTGTCAAAG	AGCAGTCTGC	CATCATGTGG	600
ATATAAATGG	ACTATGTAAA	GTGACATGGT	GCTTAACCTC	TACCTAATAA	TAGCCTCCCT	660
CCTGTTCCAA	CAAGATAACC	AACAGGTATA	TTTAATTAC	CAGTTAATAT	GTTTGGATA	720
ATGGGCTGCC	TTGAAATGCT	ATATGTTTA	TAGTACATCA	TAGCTTACT	TTTCTTCATA	780
AGGAAATTAC	AGTTACATCC	TGGCTAACAT	GGTGAACACTC	CATCTCTACT	AAAATACAA	840
AAAATTAGCC	GGGGCGTGGTG	GGGGGCACCT	GTAGTCCCAG	CTACTCGGGA	GGCTGAGGCA	900
GGAGAATGGC	GTGAACCCAG	GAGGCGGAGG	TTGCAGTGAG	CCGAGATCGT	GCCACTGTAC	960
TCTGGCTGG	GAGACAGAGC	GAGACTCCAT	CTCAAAAAAA	AAAAAAAGA	AAAAAAAGA	1020
GAGAGAGAGA	CCTGGAGTAG	AGATTCTGTC	AAAGAACCTT	TTCTTCTTG	AGAAGCATTCT	1080
GAAATGGAAT	CTGTTGTCTC	TTCGAAATAT	GTACTGCTGT	AACAGTGAAA	CAACCCCTCAG	1140
AGTATGCCTT	CGTGTGGGCT	ACTCGTTGT	GTGTTGAAC	TGGGGAAACT	GTCTGTGTT	1200
GGGTCAAGAA	TATGCAACTG	GCTGGGCACA	TTGGCTCACG	CCTGTAATCC	CAGCAATTG	1260
GGAGGCTGAG	GCAGGCGGAT	CACCTGAGGT	CAGGGCTTCA	AGACCAGACT	GGCCAACATG	1320
GTGAAACCCC	GTCTCTACTG	AAAATACAAA	AATTAGCTGG	GCATGGTGGC	AGGTGCCTGT	1380
AATCCCAGCT	ACTCGGGAGG	CTGACGTGAG	AGAATCGCTT	GAACCCGGGA	GTTGGAGGTT	1440
GCAGTGAGCC	GAGATTGCAC	CATTGCACTC	CAGCTGGGC	AAACAAGAGTG	AAACTCTTGT	1500
CTCAG						

## SEQ ID NO:8 Seq ID NO: 8 DNA sequence

Nucleic Acid Accession #: see Table 25 &amp; 25A for complete list

1	11	21	31	41	51	
GACTAGGCTG	GGCAACATAG	TGAGACCTCA	TCTCTAAAAT	TAaaaaaaaATA	AAAGCCACCA	60
GAAAAAAACC	AAAAAACATG	CCAAGTGACA	TCAGTCTTTG	ATGAAAATGG	CAGCAGAAGA	120
GTGATGCCAT	GGGTGGGGT	GGGAAATGCT	ATTTCAGCAG	AGAGGGAGCT	GTCATGGAAG	180
ACACCATGTG	GCTGGGCACG	GTGGCTCACCA	CCTGTAATCC	CAGCACTTTG	GGAGATAGAG	240
GCAGGTGGAT	CCCTTGAGCT	TAGGAATTG	AGACTAGCCT	GGGCAATAAG	AGTGAAACTC	300
CATCTCAAAA	AAAAAAAAGA	AAAAGGTGC	ATGAAACATA	TGAAGCAAAA	AGTGAAAGTC	360
CCCATTCTT	TCCTTTTCC	AGAGGTGATT	TTTGTGGCCA	ATCTGGTTTC	ATTCCCTCCC	420
AGACACTTT	CTAGGCATCT	ATGCGCCTCT	ATTACACATAT	AAACAAAATA	GGAGTTTCC	480
TGTGCTTCCC	TTAAATGGCA	TATGTATCTT	TCACTCTTTT	TTTCACCTA	GTGGATCTT	540
AATACCTAA	AAGCTCAACC	TGGGCTTGGT	GCGGTGGCTC	ATACGTGTAA	TCCCAGGCCT	600
TTGGGAGGCC	AAGTGGGAG	GATCACTTGA	GCTCAGGAGT	TCCAGACCAT	TCCAAAGCAA	660
AAACAAAAGG	ATTTGAGAT	CAGTGTGGG	AACTTAGCAA	AACACCATCT	CTTAAAAAAA	720
AAAAAAAAAA						

## SEQ ID NO:9 Seq ID NO: 9 DNA sequence

Nucleic Acid Accession #: BC010433.1

Coding sequence: 3-335

1	11	21	31	41	51	
GGTCGCCCTC	CGTCGTGGTC	TGGCGTGTAT	TCCGAGCCTT	GGTGTCTGGC	GGTTTCCGAG	60
CGTTGGTGTG	TGGCGGTTTC	CGAGCGTTGG	TGTCTGGCGG	TTTCCGACCG	TTGGTGTCTG	120
GGGTTTCCG	ACCGTTGGTG	TCTGGCACGC	GCCACCCCTCT	CTTGCTTTGG	TTGCGCCATG	180
CCGATGTACC	AGACAAGAAG	ACAAGAAAAT	GATTGAGGA	CAGCTTCAAT	CCGGTGTGA	240
AGAAGAAAGC	AGCAAAACGA	CCACTGAAAAA	CAACGCCGGT	GGAAAATAT	CCAAAGAAAG	300
GGTCCAAGC	GGTACATCGT	CATAGCCGGA	AACAGTCAGA	GCCACCAGCC	AATGATCTT	360
TCAAATGCTG	GAAAGCTGCC	AAAAGTGACA	TGCAGCACCG	AGAAGTCCGC	GTGAAGTGC	420
TGAAGGCTCT	GAAAGGGCTG	TACGGTAACC	GGGACCTGAC	CGCACGCC	GAGCTCTTC	480
CTGGCCGCTT	CAAGGACTGG	ATGGTTTCCA	TGATCATGGA	CAGAGAGTAC	AGTGTGGCAG	540
TGGAGGCCGT	CAGATTACTG	ATACTTATCC	TTAAGAACAT	GGAAGGGGTG	CTGATGGACG	600
TGGACTGTGA	GAGCGCTAC	CCCATTGTGT	AGGCCCTCTAA	TTGAGGCCTG	GCCTCTGCTG	660
TGGGTGAATT	TCTGTACTGG	AAACTTTCT	ACCCGTAGTG	CGAGATAAGA	ACGATGGGTG	720
GAAGAGAGCA	ACGCCAGAGC	CCAGGTGCC	AGAGGACTTT	CTTCCAGCTT	CTGCTGTCT	780
TCTTGTGGA	GAGCAAGCTC	CACGACCACG	CTGCTTACTT	AGTAGACAAAC	CTGTGGGACT	840
GTGCAGGGAC	TCAGCTGAAG	GACTGGGAGG	GTCTGACAAG	CCTGCTGCTG	GAGAACGGACC	900
AGAGCACGTG	CCACATGGAG	CCAGGGCCAG	GGACCTTCCA	CCTCCTAGGG	TGAAACCAGG	960
AGAGATTGCT	TGCTTCACTT	GTACAAGGCA	GGAACGGTGG	CATGGGGTGG	GGGAAACTTG	1020
GAGTTGGAAG	GTGGCTAAC	TTTGATTCTA	TGTTTTTGAT	CCTCCTGGCA	CTCCAGACCT	1080
GGGTGATGTG	CAGGAGAGCA	CACTGATAGA	AATCCTTGTG	TCCAGTCCCC	AGCAACTCCT	1140
GCCTCAGCCT	CCCGGAGCAGC	TGGGACTACA	GGGGCCCGCC	ACCACGCC	GCTAACTTT	1200
TTGTGTTTT	AGTAGAGACG	GGTTTCACC	GTGTTGGCCA	GGATGGTCTT	GATCTCTTG	1260
CCTTGTGATC	CACCTGCCTC	ATCATCCAA	AGTGCTGGGA	TTACAGGCGT	GAGCCACTGC	1320
GCCCCAGCATG	TTAGACAATT	TTAATTCT	CCTCTCTGTG	CTGTTGTTT	CTCAGCTGTG	1380
AAAGGAATAT	TCTGGTGGGG	ACAAGGTTAC	AGAGTTGCTG	AGAGGGTCTC	ATGACATGAA	1440
GGTACTGGCC	TTGGCACAGT	GCCTGGGGGG	GCGGGGACTC	CGCACATGCC	TGTGATGTCA	1500
CAGTTACTGT	CAGTCACAG	CGAACCTTCC	CTCCTTTTCC	TGTTGACTTT	CCCACACTCC	1560
TGTAACCCTC	CCTCCCTCCC	TTCTCCCTCT	CTCTCTCTCT	CACTCACGCA	CACGCACACA	1620
CACACACACA	CACACACACA	CACACACTCC	ATTCACTGTC	TCCATGACTC	TGGAGTAAAC	1680
TAACGTCTG	AGTTGCCATT	GGAAGCCCCG	TTGTCCTCAT	TTAGACTTT	ATGGGTTATA	1740
GGCCTTTG	ACTTCCCTGGG	GTCCCTTCTC	AGTTAAAAAA	AAAATTAGA	AAATTAGGC	1800
GGGCGTGGTG	GCACATGCCT	GTAATCCAG	CACCTTGGCC	TCCCAAAGTG	CTGGGATTAC	1860
AGGAGTGAGC	CACCATGCC	AGCCTCCGTT	GTCCTCATTT	AGACTTCA	GGGTTATAGG	1920
CACTTTGAC	TTCCCTGGGGT	CCTTCTTCAG	TTAAAAAAA	AAAAAAA	AAAAAAA	

SEQ ID NO:10 Seq ID NO: 10 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
AGTGGNTCCC	CCGGNCTGCA	GGAATTCCGGC	ACGAGATCAT	GATGGCTAAT	ATTCCTGAG	60
CACCTTTCAT	TCAGGCATGA	TGCCAGGTGC	ACCAACTTAC	TTAACCTCTA	TAGCCACCAC	120
CTGAGCAAGC	TCCTGTTTTA	TAAATGGACC	AGTCTTGTT	GCTGTTGTAC	AAGTTATT	180
CTTTCTATAA	CGTCCTCCTT	GTCCTCCTTC	CACATTCTTA	AAGAAACTTT	CCCTTCCTTT	240
AAAGTACTCA	GGGAGCCCTG	CATTGCTTCT	TGAAGCCTTC	TCCAGCTTCA	TCATCTCAC	300
GTGGTCTCTC	TTTTCACTAA	ATGTCCAATA	TGCTGCACAT	AAAGTACCCCA	AAGTTAGCAC	360
AGGAATTGTT	CCATGGCTGT	CATATATGTT	AAAATCATT	AAAAGTTCAT	TTTTTCTCTC	420
ATTATGGGAA	GGATACATGC	TCCTACTAGT	AAATTTAGTA	GGTAGAAAAAA	AATTATCACT	480
ATCTAGACTG	CTTCCATT	AGTCTTATG	CATAGCTTTC	GTGCTGCCT	ATTTTACCT	540
TGTGTTTGT	ACTTACTATT	ATAAAATATG	CGTCTCTATG	TTCATTGTCA	ACGATTATT	600
ACAATAACAT	GGAGTGGATT	TACATGTATT	CTCTATATT	GGATTAAAGG	AGATAGAGTA	660
TGTGAAATT	AATGGGAGAA	GTATCTGATA	CATAACAGGC	AATACAAATA	TTATCACATA	720
GCGTCAATT	ATTTGTGAAT	ATTGAAAGCT	CCAAAAAAGA	AAAAAAAGTT	TTTTTTAATT	780
CCCGTAATTA	CTTATTGCAG	TATTGTGTT	ATACAAACTG	CTCAGTCATT	TTGGAGAAAT	840
AACAATTTT	TCCTCATCA	TGAAGTAAGG	TATGCTCACT	GCAAAAAAAA	TCTAGAAAAT	900
AAAGAGGAAC	ATGCTAAAGA	AAAGAATACT	CCCATAATAAT	CTCTGTCTTC	ATAAATAATC	960
TTTGTAAACG	CTTATACACT	GCTGGTGGGA	ATGTAATT	GTTCAGCCAT	TGTGAAAAGT	1020
AGCGTAGCAA	TTCCCTGAAA	AACTTAAAT	AGATTTACCG	TTCAACCCAG	CAATCCCATT	1080
ATTGGGCATA	TACCCAGTGG	AATGTAAATC	ATCCTGCCAT	AAAACACAT	GCACATGTAT	1140
GTTCATTGCA	GCACATTTC	CAATAGCAAA	GACATGGAAT	CAACCTATAT	GCCCCATCAAT	1200
AGTAGACTGA	ATAAAGAAAAA	TATGGTACAT	ATTCAACCACA	GAATACTAAG	CAGCCATAAA	1260
	AAAAAA					

SEQ ID NO:11 Seq ID NO: 11 DNA sequence

Nucleic Acid Accession #: NM\_000582.1

Coding sequence: 88-990

1	11	21	31	41	51	
GCAGAGCACA	GCATCGTCGG	GACCAGACTC	GTCTCAGGCC	AGTTGCAGCC	TTCTCAGCCA	60
AACGCCGACC	AAGGAAAAC	CACTACCATG	AGAATTGCAG	TGATTTGCTT	TTGCCTCC	120
GGCATCACCT	GTGCCATACC	AGTTAAACAG	GCTGATTCTG	GAAGTTCTGA	GGAAAAGCAG	180
CTTTACAACA	AATACCCAGA	TGCTGTGGCC	ACATGGCTAA	ACCCTGACCC	ATCTCAGAAG	240
CAGAATCTCC	TAGCCCCACA	GACCCTTCCA	AGTAAGTCCA	ACGAAAGCCA	TGACCACATG	300
GATGATATGG	ATGATGAA	TGATGATGAC	CATGTGGACA	GCCAGGACTC	CATTGACTCG	360
AACGACTCTG	ATGATGTAGA	TGACACTGAT	GATTCTCACC	AGTCTGATGA	GTCTCACCAT	420
TCTGATGAAT	CTGATGAACT	GGTCACTGAT	TTTCCCACGG	ACCTGCCAGC	AACCGAAGTT	480
TTCACTCCAG	TTGTCCCCAC	AGTAGACACA	TATGATGGCC	GAGGTGATAG	TGTGGTTTAT	540
GGACTGAGGT	CAAAATCTAA	GAAGTTTCG	AGACCTGACA	TCCAGTACCC	TGATGCTACA	600
GACGAGGACA	TCACCTCACA	CATGGAAAGC	GAGGAGTTGA	ATGGTGCATA	CAAGGCCATC	660
CCCGTTGCC	AGGACCTGAA	CGCGCCTCT	GATTGGGACA	GCCGTGGAA	GGACAGTTAT	720
GAAACGAGTC	AGCTGGATGA	CCAGAGTGCT	GAAACCCACA	GCCACAAGCA	GTCCAGATTA	780
TATAAGCGGA	AAGCCAATGA	TGAGAGCAAT	GAGCATTCCG	ATGTGATTGA	TAGTCAGGAA	840
CTTTCCAAAG	TCAGCCGTGA	ATTCCACAGC	CATGAATTTC	ACAGCCATGA	AGATATGCTG	900
GTTGTAGACC	CCAAAAGTAA	GGAAGAAGAT	AAACACCTGA	AATTCTGTAT	TTCTCATGAA	960
TTAGATAGTG	CATCTTCTGA	GGTCAATTAA	AAGGAGAAAA	AATACAATT	CTCACTTTGC	1020
ATTTAGTC	AAGAAAAAAAT	GCTTTATAGC	AAAATGAAAG	AGAACATGAA	ATGCTTCTTT	1080
CTCAGTTTAT	TGGTTGAATG	TGTATCTATT	TGAGTCTGGA	AATAACTAAT	GTGTTTGATA	1140
ATTAGTTTAG	TTTGTGGCTT	CATGGAAACT	CCCTGTAAAC	AAAAGCTTC	AGGGTTATGT	1200
CTATGTTCAT	TCTATAGAAG	AAATGCAAAC	TATCACTGTA	TTTTAATATT	TGTTATTCTC	1260
TCATGAATAG	AAATTATGT	AGAAGCAAAC	AAAATACTTT	TACCCACTTA	AAAAGAGAAT	1320
ATAACATTT	ATGTCACTAT	AATCTTTGT	TTTTAAGTT	AGTGTATATT	TTGTTGTGAT	1380
TATCTTTTG	TGGTGTGAAT	AAATCTTTA	TCTTGAATGT	AATAAGAATT	TGGTGGTGTC	1440
AATTGTTAT	TTGTTTCCC	ACGGTTGTCC	AGCAATTAAAT	AAAACATAAC	CTTTTTACT	1500
	GCCTAAAAAA	AAAAAAAAAA	AAAA			

SEQ ID NO:12 Seq ID NO: 12 Protein sequence:

Protein Accession #: NP\_000573.1

1	11	21	31	41	51	
MRIAVICFCL	LGITCAIPVK	QADSGSSEEK	QLYNKYPAV	ATWLNPDP	SQ KQNLLAPQTL	60
PSKSNEHDH	MDDMDDEDDD	DHVDSQDSID	SNDSDDVDDT	DDSHQSDESH	HSDESDELVT	120
DFPTDLPATE	VFTPVVPTVD	TYDGRGDSVV	YGLRSKSKKF	RRPDIQYPDA	TDEDITSHME	180
SEELNGAYKA	IPVAQDLNAP	SDWDSRGKDS	YETSQLDDQS	AETHSHKQSR	LYKRKANDES	240
NEHSDVIDSQ	ELSKVSREFH	SHEFHSHEDM	LVVDPKSKEE	DKHLKFRISH	ELDSASSEVN	

SEQ ID NO:13 Seq ID NO: 13 DNA sequence

Nucleic Acid Accession #: NM\_001793

Coding sequence: 71-2560

1	11	21	31	41	51	
AAAGGGGCAA	GAGCTGAGCG	GAACACCGGC	CCGCCGTGCG	GGCAGCTGCT	TCACCCCTCT	60
CTCTGCAGCC	ATGGGGCTCC	CTCGTGGACC	TCTCGCGTCT	CTCCTCCTTC	TCCAGGTTTG	120
CTGGCTGCAG	TGCGCGGCCT	CCGAGCCGTG	CCGGGCGGTC	TTCAGGGAGG	CTGAAGTGAC	180
CTTGGAGGCG	GGAGGCGCGG	AGCAGGAGCC	CGGCCAGGCG	CTGGGGAAAG	TATTCATGGG	240
CTGCCCTGGG	CAAGAGCCAG	CTCTGTTTAG	CACTGATAAT	GATGACTTCA	CTGTGCGGAA	300
TGGCGAGACA	GTCCAGGAAA	GAAGGTCACT	GAAGGAAAGG	AATCCATTGA	AGATCTTCCC	360
ATCCAAACGT	ATCTTACGAA	GACACAAGAG	AGATTGGGTG	GTTGCTCCAA	TATCTGTCCC	420
TGAAAATGGC	AAGGGTCCCT	TCCCCAGAG	ACTGAATCAG	CTCAAGTCTA	ATAAAGATAG	480
AGACACCAAG	ATTTTCTACA	GCATCACGGG	GCCGGGGGCA	GACAGCCCCC	CTGAGGGTGT	540
CTTCGCTGTA	GAGAAGGGAGA	CAGGCTGGTT	GTTGTTGAAT	AAGCCACTGG	ACCGGGAGGA	600
GATTGCCAAC	TATGAGCTCT	TTGGCCACGC	TGTGTCAGAG	AATGGTGCCT	CAGTGGAGGA	660
CCCCATGAAC	ATCTCCATCA	TCGTGACCGA	CCAGAATGAC	CACAAGCCC	AGTTTACCCA	720
GGACACCTTC	CGAGGGAGTG	TCTTAGAGGG	AGTCCTACCA	GGTACTTCTG	TGATGCAGGT	780
GACAGCCACG	GATGAGGATG	ATGCCATCTA	CACTTACAAT	GGGGTGGTTG	CTTACTCCAT	840
CCATAGCCAA	GAACCAAAGG	ACCCACACGA	CCTCATGTT	ACCATTCA	GGAGCACAGG	900
CACCATCAGC	GTCATCTCCA	GTGGCCTGGA	CCGGGAAAAAA	GTCCCTGAGT	ACACACTGAC	960
CATCCAGGCC	ACAGACATGG	ATGGGGACGG	CTCCACCA	ACGGCAGTGG	CAGTAGTGG	1020
GATCCTTGTAT	GCCAATGACA	ATGCTCCCAT	GTTTGACCCC	CAGAAGTACG	AGGCCATGT	1080
GCCTGAGAAT	GCAGTGGGCC	ATGAGGTGCA	GAGGCTGACG	GTCACTGATC	TGGACGCC	1140
CAACTCACCA	GCCTGGCGTG	CCACCTACCT	TATCATGGGC	GGTGACGACG	GGGACCATTT	1200
TACCATCACC	ACCCACCCCTG	AGAGCAACCA	GGGCATCCTG	ACAACCAGGA	AGGGTTTGG	1260
TTTGAGGCC	AAAAACCAGC	ACACCCCTGA	CGTGAAGTG	ACCAACGAGG	CCCCTTTGT	1320
GCTGAAGCTC	CCAACCTCCA	CAGCCACCAT	AGTGGTCCAC	GTGGAGGATG	TGAATGAGGC	1380
ACCTGTGTT	GTCCCACCC	CCAAAGTCGT	TGAGGTCCAG	GAGGGCATCC	CCACTGGGA	1440
GCCTGTGTGT	GTCTACACTG	CAGAAGACCC	TGACAAGGAG	AATCAAAGA	TCAGCTACCG	1500
CATCCTGAGA	GACCCAGCAG	GGTGGCTAGC	CATGGACCCA	GACAGTGGGC	AGGTACACAGC	1560
TGTGGCACC	CTCGACCGTG	AGGATGAGCA	GTTGTGAGG	AACAACATCT	ATGAAGTCA	1620
GGTCTTGGCC	ATGGACAATG	GAAGCCCTCC	CACCACTGGC	ACGGGAACCC	TTCTGCTAAC	1680
ACTGATTGAT	GTCAATGACC	ATGGCCCA	CCCTGAGCCC	CGTCAGATCA	CCATCTGCAA	1740
CCAAAGCCCT	GTGCCGCCAG	TGCTGAACAT	CACGGACAAG	GACCTGTCTC	CCCACACCTC	1800
CCCTTCCAG	GCCCCAGCTCA	CAGATGACTC	AGACATCTAC	TGGACGGCAG	AGGTCAACGA	1860
GGAAGGGTAC	ACAGTGGTCT	TGTCCCTGAA	GAAGTTCTG	AAGCAGGATA	CATATGACGT	1920
GCACCTTCTC	CTGTCTGACC	ATGGCAACAA	AGAGCAGCTG	ACGGTGATCA	GGGCCACTGT	1980
GTGCGACTGC	CATGCCATG	TCGAAACCTG	CCCTGGACCC	TGGAAGGGAG	TTTCATCCT	2040
CCCTGTGCTG	GGGGCTGTCC	TGGCTCTGCT	GTTCCCTCCTG	CTGGTGCTGC	TTTTGTTGGT	2100
GAGAAAGAAAG	CGGAAGATCA	AGGAGCCCT	CCTACTCCCA	GAAGATGACA	CCCGTGACAA	2160
CGTCTTCTAC	TATGGCGAAG	AGGGGGTGG	CGAAGAGGAC	CAGGACTATG	ACATCACCCA	2220
GCTCCACCGA	GGTCTGGAGG	CCAGGCCGA	GGTGGTTCTC	CGCAATGACG	TGGCACCAAC	2280
CATCATCCCC	ACACCCATGT	ACCGTCCTCG	GCCAGCCAAC	CCAGATGAA	TCGGCAACTT	2340
TATAATTGAG	AACCTGAAGG	CGGCTAACAC	AGACCCCCACA	GCCCCGCCCT	ACGACACCT	2400
CTTGGTGTTC	GACTATGAGG	GCAGCGGCTC	CGACGCCGCG	TCCCTGAGCT	CCCTCACCTC	2460
CTCCGCCTCC	GACCAAGACC	AAGATTACGA	TTATCTGAAC	GAGTGGGGCA	GCCGCTTCAA	2520
GAAGCTGGCA	GACATGTACG	GTGGCGGGGA	GGACGACTAG	GGGGCCTGCC	TGCAGGGCTG	2580

GGGACCAAAC	GTCAGGCCAC	AGAGCATCTC	CAAGGGTCT	CAGTTCCCCC	TTCAGCTGAG	2640
GA <del>CTT</del> CGGAG	CTTGT <del>C</del> AGGA	AGTGGCC <del>T</del> A	GCAACT <del>T</del> GGC	GGAGACAGGC	TATGAGTC <del>T</del> G	2700
ACGTTAGAGT	GGTTGCTTCC	TTAGCCTTC	AGGATGGAGG	AATGTGGGCA	GTTTGACTTC	2760
AGCACTGAAA	ACCTCTCCAC	CTGGGCCAGG	GTTGCCTCAG	AGGCCAAGTT	TCCAGAA <del>G</del> CC	2820
TCTTACCTGC	CGTAAAATGC	TCAACCCTGT	GTCCTGGGC	TGGGCCTGCT	GTGACTGACC	2880
TACAGTGGAC	TTTCTCTCTG	GAATGGAACC	TTCTTAGGCC	TCCTGGTGCA	ACTTAATT <del>T</del> T	2940
TTTTTTAAT	GCTATCTTCA	AAACGTTAGA	GAAAGTTCTT	CAAAGTGCA	GCCCAGAGCT	3000
GCTGGGCCA	CTGGCCGTCC	TGCATTTCTG	GTTCCAGAC	CCCAATGCCT	CCCATT <del>C</del> GG	3060
TGGATCTCTG	CGTTTTATA	CTGAGTGTGC	CTAGGTTGCC	CCTTATT <del>T</del> TTT	TATTTTCCCT	3120
GT <del>T</del> CGT <del>T</del> GC	TATAGATGAA	GGGTGAGGAC	AATCGTGTAT	ATGTACTAGA	ACTTTTTAT	3180
TAAAGAAACT	TTTCCCAGAA	AAAAAA				

SEQ ID NO:14 Seq ID NO: 14 Protein sequence:

Protein Accession #: NP\_001784.2

1	11	21	31	41	51	
MGLPRGPLAS	LLLLQVCWLQ	CAASEPCRAV	FREAEVTLEA	GGAEQE <del>P</del> QQA	LGKVFMGCPG	60
QEPALFSTDN	DDFTVRNGET	VQERRSLKER	NPLKIFPSKR	ILRRHKRDWV	VAPISVPENG	120
KGPFPQR <del>L</del> NQ	LKS <del>N</del> KDRDTK	IFYSITGPG <del>A</del>	DSPPEGVFAV	EKETGWLLL <del>N</del>	KPLDREEIAK	180
YELFGH <del>A</del> VSE	NGASVEDPMN	ISIIVTDQND	HKP <del>K</del> F <del>T</del> QDTF	RGSVLEGVLP	GTSVMQVTAT	240
DEDDAIYT <del>Y</del> N	GVVAYSIHSQ	EPKD <del>P</del> HDLMF	TIHRSTGTIS	VISSGLDREK	VPEYTLTIQA	300
TDMDGDGSTT	TAVAVVEILD	ANDNAPMFDP	QKYEAHV <del>P</del> EN	AVGHEVQRLT	VTLD <del>D</del> APNSP	360
AWRATY <del>L</del> IMG	GDDGDHFTIT	THPESNQGIL	TTRKG <del>L</del> DFEA	KNQHTLYVEV	TNEAPFVLKL	420
PTSTATIVVH	VEDVNEAPVF	VPPSKVVEVQ	E <del>I</del> GIPTGE <del>P</del> VC	VYTAEDPDKE	NQKISYRILR	480
DPAGWLAMDP	DSGQV <del>T</del> AVGT	LDREDEQFVR	NNIYEVMVLA	MDNGSPPTTG	TG <del>T</del> LLLT <del>L</del> ID	540
VNDHGPVPEP	RQITICQN <del>S</del> P	VRQVLNITDK	DLS <del>P</del> H <del>T</del> SPFQ	AQLTDDSDIY	WTAEVNEEGD	600
TVVLSLKKFL	KQDTYDVHLS	LSDHGNKEQL	TVIRATVCDC	HGHVETCPGP	WKGGFILPVL	660
GAVLALLFLL	LV <del>LLL</del> VRKK	RKI <del>K</del> EPLL <del>P</del>	EDDTRDNV <del>F</del> Y	YGEEGGGEED	QDYDITQLHR	720
GLEARPEVVL	RNDVAP <del>T</del> IIP	TPM <del>Y</del> RP <del>R</del> PAN	PDEIGNFIIE	NLKAANTDPT	APPYDTLLVF	780
DYEGSGSDAA	SLSSLTSSAS	DQDQDYDYL <del>N</del>	EWGSRFKKLA	DMYGGEDD		

SEQ ID NO:15 Seq ID NO: 15 DNA sequence

Nucleic Acid Accession #: XM\_051860.2

Coding sequence: 261-4346

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GAGCTAGCGC	TCAAGCAGAG	CCCAGGCCG	TGCTATCGGA	CAGAGCCTGG	CGAGGGCAAG	60
CGGCGCGGGG	AGCCAGCGGG	GCTGAGCGCG	GCCAGGGTCT	GAACCCAGAT	TTCCCAGACT	120
AGCTACCACT	CCGCTTGCCC	ACGCCCCGGG	AGCTCGCGC	GCCTGGCGGT	CAGCGACCAG	180
ACGTCCGGGG	CCGCTGCGCT	CCTGGCCCGC	GAGGC <del>G</del> TGAC	ACTGTCTCGG	CTACAGACCC	240
AGAGGGAGCA	CACTGCCAGG	ATGGGAGCTG	CTGGGAGGCA	GGACTTCC <del>T</del> C	TTCAAGGCCA	300
TGCTGACCAT	CAGCTGGCTC	ACTCTGACCT	GCTTCCCTGG	GGCCACATCC	ACAGTGGCTG	360
CTGGGTGCC	TGACCAGAGC	CCTGAGTTGC	AACCCTGGAA	CCCTGGCCAT	GACCAAGACC	420
ACCATGTGCA	TATCGGCCAG	GGCAAGACAC	TGCTGCTCAC	CTCTTCTGCC	ACGGTCTATT	480
CCATCCACAT	CTCAGAGGGA	GGCAAGCTGG	TCATTAAAGA	CCACGACGAG	CCGATTGTTT	540
TGCGAACCCG	GCACATCCTG	ATTGACAACG	GAGGAGAGCT	GCATGCTGGG	AGTGCCCTCT	600
GCCCTT <del>T</del> CCA	GGGCAATTTC	ACCATCATT	TGTATGGAAG	GGCTGATGAA	GGTATT <del>C</del> AGC	660
CGGATCCTTA	CTATGGTCTG	AAGTACATTG	GGGT <del>T</del> GGTAA	AGGAGGCGCT	CTTGAGTTGC	720
ATGGACAGAA	AAAGCTCTCC	TGGACATTTC	TGAACAAGAC	CCTTCACCCA	GGTGGCATGG	780
CAGAAGGAGG	CTATTTTTT	GAAAGGAGCT	GGGGCCACCG	TGGAGTTATT	GTTCATGTCA	840
TCGACCCAA	ATCAGGCACA	GTCATCCATT	CTGACCGGTT	TGACACCTAT	AGATCCAAGA	900
AAGAGAGTGA	ACGTCTGGTC	CAGTATT <del>T</del> GA	ACGCGGTGCC	CGATGGCAGG	ATCCTTCTG	960
TTGCAGTGAA	TGATGAAGGT	TCTCGAAATC	TGGATGACAT	GGCCAGGAAG	GGGATGACCA	1020
AATTGGGAAG	CAAACACTTC	CTGCACCTT <del>G</del>	GATTAGACA	CCCTTGGAGT	TTTCTAACTG	1080
TGAAAGGAAA	TCCATCATCT	TCAGTGGAAAG	ACCATATTGA	ATATCATGGA	CATCGAGGCT	1140
CTGCTGCTGC	CCGGGTATT <del>C</del>	AAATTGTCC	AGACAGAGCA	TGGCGAATAT	TTCAATGTTT	1200
CTTGTCCAG	TGAGTGGTT	CAAGACGTGG	AGTGGACGGA	GTGGTCGAT	CATGATAAAG	1260

TATCTCAGAC	TAAAGGTGGG	GAGAAAATTT	CAGACCTCTG	GAAAGCTCAC	CCAGGAAAAA	1320
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AGGTTGTCTA	CAAAAAAAGGC	CAGGATTATA	GGTTTGCTTG	CTACGACCGG	GCGAGAGCCT	1440
GCCGGAGCTA	CCGTGTACGG	TTCCCTGTG	GGAAAGCCTGT	GAGGCCAAA	CTCACAGTCA	1500
CCATTGACAC	CAATGTGAAC	AGCACCATT	TGAACATTGGA	GGATAATGTA	CAGTCATGGA	1560
AACCTGGAGA	TACCCCTGGTC	ATTGCCAGTA	CTGATTACTC	CATGTACAG	GCAGAAGAGT	1620
TCCAGGTGCT	TCCCTGCAGA	TCCTGCGCCC	CCAACCAGGT	CAAAGTGGCA	GGGAAACCAA	1680
TGTACCTGCA	CATCGGGGAG	GAGATAGACG	GCGTGGACAT	GCGGGCGGAG	GTGGGGCTTC	1740
TGAGCCGGAA	CATCATAGTC	ATGGGGGAGA	TGGAGGACAA	ATGCTACCCC	TACAGAAACC	1800
ACATCTGCAA	TTTCTTTGAC	TTCGATACCT	TTGGGGGCCA	CATCAAGTTT	GCTCTGGGAT	1860
TTAAGGCAGC	ACACTTGGAG	GGCACGGAGC	TGAAGCATAT	GGGACAGCAG	CTGGTGGGTC	1920
AGTACCCGAT	TCACTTCCAC	CTGGCCGGTG	ATGTAGACGA	AAGGGGAGGT	TATGACCCAC	1980
CCACATACAT	CAGGGACCTC	TCCATCCATC	ATACATTCTC	TCGCTGCGTC	ACAGTCCATG	2040
GCTCCAATGG	CTTGTGATC	AAGGACGTTG	TGGGCTATAA	CTCTTGGC	CACTGTTCT	2100
TCACGGAAGA	TGGGCCGGAG	GAACGCAACA	CTTTTGACCA	CTGTCTTGGC	CTCCTTGTCA	2160
AGTCTGGAAC	CCTCCCTCCCC	TCGGACCGTG	ACAGCAAGAT	GTGCAAGATG	ATCACAGAGG	2220
ACTCCTACCC	GGGGTACATC	CCCAAGCCA	GGCAAGACTG	CAATGCTGTG	TCCACCTTCT	2280
GGATGGCCAA	TCCCAACAAAC	AACCTCATCA	ACTGTGCCGC	TGCAGGATCT	GAGGAAACTG	2340
GATTTTGGTT	TATTTTCAC	CACGTACCAA	CGGGCCCCCTC	CGTGGGAATG	TACTCCCCAG	2400
GTTATTTCAGA	GCACATTCCA	CTGGGAAAAT	TCTATAACAA	CCGAGCACAT	TCCAACCTACC	2460
GGGCTGGCAT	GATCATAGAC	AACGGAGTC	AAACCACCGA	GGCCTCTGCC	AAGGACAAGC	2520
GGCCGTTCT	CTCAATCATC	TCTGCCAGAT	ACAGCCCTCA	CCAGGACGCC	GACCCGCTGA	2580
AGCCCCGGGA	GCGGCCATC	ATCAGACACT	TCATTGCCTA	CAAGAACCGAG	GACCACGGGG	2640
CCTGGCTGCG	CGGCGGGGAT	GTGTGGCTGG	ACAGCTGCCG	GTGGCTGAC	AATGGCATTG	2700
GCCTGACCCCT	GGCCAGTGGT	GGAACCTTCC	CGTATGACGA	CGGCTCCAAG	CAAGAGATAA	2760
AGAACAGCTT	GTGGTGTGGC	GAGAGTGGCA	ACGTGGGAC	GGAAATGATG	GACAATAGGA	2820
TCTGGGGCCC	TGGCGGCTTG	GACCATAGCG	GAAGGACCCCT	CCCTATAGGC	CAGAATTTTC	2880
CAATTAGAGG	AATTCAGTTA	TATGATGGCC	CCATCAACAT	CCAAAACCTGC	ACTTTCCGAA	2940
AGTTTGTGGC	CCTGGAGGGC	CGGCACACCA	GCGCCCTGGC	CTTCCGCCCTG	AATAATGCCT	3000
GGCAGAGCTG	CCCCCATAAC	AACGTGACCG	GCATTGCCCT	TGAGGACGTT	CCGATTACTT	3060
CCAGAGTGT	CTTGGGAGAG	CCTGGGCCCT	GGTCAACCA	GCTGGACATG	GATGGGGATA	3120
AGACATCTGT	GTTCCATGAC	GTCGACGGCT	CCGTGTCCGA	GTACCCCTGGC	TCCTACCTCA	3180
CGAAGAATGA	CAACTGGCTG	GTCCGGCACCC	CAGACTGCAT	CAATGTTCCC	GACTGGAGAG	3240
GGGCCATTG	CAGTGGGTGC	TATGCACAGA	TGTACATTCA	AGCCTACAAG	ACCAGTAACC	3300
TGCGAATGAA	GATCATCAAG	AATGACTTCC	CCAGCCACCC	TCTTTACCTG	GAGGGGGCGC	3360
TCACCAGGAG	CACCCATTAC	CAGCAATACC	AACCGGTTGT	CACCCCTGAG	AAGGGCTACA	3420
CCATCCACTG	GGACCCAGACG	GCCCCCGCCG	AACTCGCCAT	CTGGCTCATC	AACTTCAACA	3480
AGGGCGACTG	GATCCGAGTG	GGGCTCTGCT	ACCCCGCGAGG	CACCACATT	TCCATCCTCT	3540
CGGATGTTCA	CAATCGCCTG	CTGAAGCAAA	CGTCCAAGAC	GGGCGTCTTC	GTGAGGACCT	3600
TGCAGATGGA	CAAAGTGGAG	CAGAGCTACC	CTGGCAGGAG	CCACTACTAC	TGGGACGAGG	3660
ACTCAGGGCT	GTTGTTCTG	AAGCTGAAAG	CTCAGAACGA	GAGAGAGAAG	TTTGCTTTCT	3720
GCTCCATGAA	AGGCTGTGAG	AGGATAAAGA	TTAAAGCTCT	GATTCCAAAG	AACGCAGGGC	3780
TCAGTGAATG	CACAGCCACA	GCTTACCCCA	AGTCACCGA	GAGGGCTGTC	GTAGACGTGC	3840
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GGCAGCTTT	CAACTATGTG	GCGACCATCC	CTGACAATT	CATAGTGCTT	ATGGCATCAA	4140
AGGGAAGATA	CGTCTCCAGA	GGCCCATGGA	CCAGAGTGCT	GGAAAAGCTT	GGGGCAGACA	4200
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TCTGGGTGAC	ACTGGACACT	GAGGATCACA	AAGCCAAAAT	CTTCCAAGTT	GTGCCCATCC	4320
CTGTGGTGA	GAAGAAGAAG	TTGTGAGGAC	AGCTGCCGCC	CGGTGCCACC	TCGTGGTAGA	4380
CTATGACGGT	GACTCTTGGC	AGCAGACCG	TGGGGATGG	CTGGGCCCC	CAGCCCTG	4440
CAGCAGCTGC	CTGGGAAGGC	CGTGTTCAG	CCCTGATGGG	CCAAGGGAAG	GCTATCAGAG	4500
ACCCTGGTGC	TGCCACCTGC	CCCTACTCAA	GTGTCTACCT	GGAGCCCTG	GGCGGGTGT	4560
GGCCAATGCT	GGAAACATT	ACTTTCC	AGCCTCTTGG	GTGCTTCTCT	CCTATCTGTG	4620
CCTCTTCAGT	GGGGTTTGG	GGACCATATC	AGGAGACCTG	GGTTGTGCTG	ACAGCAAAGA	4680
TCCACTTTGG	CAGGAGCCCT	GACCCAGCTA	GGAGGTAGTC	TGGAGGGCTG	GTCATTCA	4740
GATCCCCATG	GTCTTCAGCA	GACAAGTGTG	GGTGGTAAAT	GTAGGAGAAA	GAGCCTTGGC	4800
CTTAAGGAAA	TCTTACTCC	TGTAAGCAAG	AGCCAACCTC	ACAGGATTAG	GAGCTGGGTT	4860
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AGACTTTGAG	TGGCAGGTTT	GGACTTGAC	TAGATGACTC	TCAAAGGCC	TTTAGTTCT	4980
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CCACTGATAT	CCATGATGCT	GGGTGCCCA	GCGCACACGG	GATGGAGAGG	TGAGAACTAA	5100
TGCCTAGCTT	GAGGGGTCTG	CAGTCCAGTA	GGGCAGGCAG	TCAGGTCCAT	GTGCACTGCA	5160
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GCTCAGGAAG	GCTTCTTGCT	TACAGGAATG	AAGGCTGGGG	GCATTTGCT	GGGGGGAGAT	5280
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GTGACTACGG	GGTCGCCCTT	TGCTCACGTC	TCTCTGGCCC	ACTCATGATG	GAGAAGTGTG	5400
GTCAGAGGGG	AGCAATGGC	TTTGCTGCTT	ATGAGCACAG	AGGAATTCA	TCCCCAGGCA	5460
GCCCTGCCTC	TGACTCCAAG	AGGGTGAAGT	CCACAGAAGT	GAGCTCTGC	CTTAGGGCCT	5520
CATTTGCTCT	TCATCCAGGG	AACTGAGCAC	AGGGGGCCTC	CAGGAGACCC	TAGATGTGCT	5580
CGTACTCCCT	CGGCCTGGG	TTTCAGAGCT	GGAAATATAG	AAAATATCTA	GCCCAAAGCC	5640
TTCATTTAA	CAGATGGGG	AAAGTGANCC	CCAAGATGGG	AAAGAACAC	ACAGCTAAGG	5700
GAGGGCCTGG	GGAGCCCCAC	CCTAGCCCTT	GCTGCCACAC	CACATTGCCT	CAACAACCGG	5760
CCCCAGAGTG	CCCAGGCACT	CCTGAGGTAG	CTTCTGGAAA	TGGGGACAAG	TCCCCTCGAA	5820
GGAAAGGAAA	TGACTAGAGT	AGAATGACAG	CTAGCAGATC	TCTTCCCTCC	TGCTCCCAGC	5880
GCACACAAAC	CGGCCCTCCC	CTTGGTGTG	GCGTCCCTG	TGGCCTTCAC	TTTGTTCACT	5940
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TCCTGTCCT	GCAGCTCTAC	AGGTGAGGCC	CAGCAGAGGG	AGTAGGGCTC	GCCATGTTTC	6060
TGGTGAGCCA	ATTGGCTGA	TCTTGGGTGT	CTGAACAGCT	ATTGGGTCCA	CCCCAGTCCC	6120
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GCTCCTGTAA	GAGGGAGAAC	TCTATCTGTG	GTTTATAATC	TTGCACGAGG	CACCAGAGTC	6240
TCCCTGGGTC	TTGTGATGAA	CTACATTAT	CCCCTTCCT	GCCCCAACCA	CAAACCTCTT	6300
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GAGTCCATT	CCCAGGTGGG	AGCCAACCTGT	CAGGGAGGTC	TTTCCCACCA	ACATCTTC	6420
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CCTCATGTCC	TTCTGTCCA	CGGTTTTGTT	GAGTTTCAC	TCTTCTAATG	CAAGGGTCTC	6600
ACACTGTGAA	CCACTTAGGA	TGTGATCACT	TTCAAGGTGGC	CAGGAATGTT	GAATGTCTTT	6660
GGCTCAGTTC	ATTTAAAAAA	GATATCTATT	TGAAAGTTCT	CAGAGTTGTA	CATATGTTTC	6720
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TTCTGTTTGT	AAGACTTAAG	TGAGTTAGGT	CTTAAAGGAA	AGCAACGCTC	CTCTGAAATG	6900
CTTGTCTTT	TTCTGTTGCC	GAAATAGCTG	GTCCTTTTC	GGGAGTTAGA	TGTATAGAGT	6960
GTTTGTATGT	AAACATTTCT	TGTAGGCATC	ACCATGAACA	AAGATATATT	TTCTATTAT	7020
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SEQ ID NO:16 Seq ID NO: 16 Protein sequence:

Protein Accession #: XP\_051860.2

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TIILYGRADE	GIQPDPYYGL	KYIVGVKGGA	LELHGQKKLS	WTFLNKTLHP	GGMAEGGYFF	180
ERSWGHHRGVI	VHVIDPKSGT	VIHSDRFDTY	RSKKESERLV	QYNNAVPDGR	ILSVAVNDEG	240
SRNLDDDMARK	AMTKLGSKHF	LHLGFRHPWS	FLTVKGNPSS	SVEDHIEYHG	HRGSAAARVF	300
KLFQTEHGEY	FNVSLSSSEWV	QDVEWTEWD	HDKVSQTKGG	EKISDLWKAH	PGKICNRPID	360
IQATTMDGVN	LSTEVVYKKG	QDYRFACYDR	GRACRSYRVR	FLCGKPVRPK	LTVTIDTNVN	420
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EIDGVDMRAE	VGLLSRNII	MGEAMEDKCYP	YRNHICNFFD	FDTFGGHIKF	ALGFKAHLE	540
GTELKHMQQ	LVGQYPIHFH	LAGDVDERGG	YDPPTYIRD	SIHHTFSRCV	TVHGSNGLLI	600
KDVGVGNSLG	HCFFTEDGPE	ERNTFDHCLG	LLVKGTL	SDRDSKMCKM	ITEDSYPGYI	660
PKPRQDCNAV	STFWMANPNN	NLINCAAAGS	EETGFWFIFH	HVPTGPSVGM	YSPGYSEHIP	720
LGKFYNNRAH	SNYRAGMIID	NGVKTTEASA	KDKRPFLSII	SARYSPHQDA	DPLKPREPAI	780
IRHFIAYKNQ	DHGAWLRGGD	VWLDSCRFA	NGIGLTLASG	GTFPYDDGSK	QEIKNSLFVG	840
ESGNVGTEMM	DNRIWGPGL	DHSGRTP	QNFFPIRGQL	YDGPINIQNC	TFRKFVALEG	900
RHTSALAFRL	NNAQSCP	NVTGIAFEDV	PITSRVFFGE	PGPWFNQLDM	DGDKTSVFHD	960
VDGSVSEYPG	SYLTKNDNW	VRHPDCINVP	DWRGAICSGC	YAQMYIQAYK	TSNLRMKI	1020
NDFPSHPLYL	EGALTRSTHY	QQYQPVVTLO	KGYTIHWDQT	APAELAIWLI	NFNKGDWIRV	1080

GLCYPRGTTF SILSDVHNRL LKQTSKTGVF VRTLQMDKVE QSYPGRSHYY WDEDGLLFL 1140  
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 GSQLKTKDHF LEVKMESSKQ HFFHLWNDFA YIEVDGKKYP SSEDGIQVVV IDGNQGRVVS 1260  
 HTSFRNSILQ GIPWQLFNYV ATIPDNSIVL MASKGRYVSR GPWTRVLEKL GADRGLKLKE 1320  
 QMAFGFKGS FRPIWVTLDT EDHKAKIFQV VPIPVVKKKK L

SEQ\_ID NO:17 Seq\_ID NO: 17 DNA sequence  
 Nucleic Acid Accession #: NM\_015515.1  
 Coding sequence: 61-1329

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GGCTGGGG CC	GGCCCAGGAG	CTTCCCCAGG	GCTCCCACCG	TCCATGGCGG	TGCGGGGGGA	180
GCCC CGCATCT	CCCTGTCCTT	CACCACGCGG	AGCTGCCAC	CCCCTGGAGG	GTCTTGGGT	240
TCTGGAAGAA	GCAGCCCCCT	ACTAGGGCGA	AATGGGAAGG	CCACCATGCA	GAATCTCAAC	300
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CAGTATGAGG	AAAACATCAC	ACACCTGCGA	GAGCAGATAG	TGGATGGTAA	GATGACCAAT	480
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TATGAAAATG	AACACTCCTT	TAAGAAAGAC	TTGAAATTG	AACTCGAGGG	CCTCCGAAGG	600
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ACTTGGTATA	AAGAACAGTC	TGCAGCCATG	TCCCAGGAGG	CAGCCAGTCC	AGCCACTGTG	900
CAGAGCAGAC	AAGGTGACAT	CCACGAACTG	AAGCGCACAT	TCCAGGCCCT	GGAGATTGAC	960
CTGCAGGCAC	AGTACAGCAC	GAAATCTGCT	TTGGAAAACA	TGTTATCCGA	GACCCAGTCT	1020
CGGTACTCCT	GCAAGCTCCA	GGACATGCAA	GAGATCATCT	CCCACTATGA	GGAGGAACTG	1080
ACCGAGCTAC	GCCACGAAC	GGAGCGGCAG	AACAATGAAT	ACCAAGTGCT	GCTGGGCATC	1140
AAAACCCACC	TGGAGAAGGA	AATCACCACG	TACCGACGGC	TCCTGGAGGG	AGAGAGTGAA	1200
GGGACACGGG	AAGAATCAA	GTGAGCATG	AAAGTGTCTG	CAACTCCAAA	GATCAAGGCC	1260
ATAACCCAGG	AGACCATCAA	CGGAAGATTA	GTTCTTGTGTC	AAGTGAATGA	AATCCAAAAG	1320
CACGCATGAG	ACCAATGAAA	GTTTCCGCC	GTTGTAAAGT	CTATTTCCC	CCAAGGAAAG	1380
TCCTTGCACA	GACACCAGTG	AGTGAGTTCT	AAAAGATACC	CTTGGAAATTA	TCAGACTCAG	1440
AAACTTTTAT	TTTTTTTTT	CTGTAACAGT	CTCACCAAGAC	TTCTCATATA	GCTCTTAATA	1500
TATTGCACTT	TTCTAATCAA	AGTGCAGGTT	TATGAGGGTA	AAGCTCTACT	TTCTACTGC	1560
AGCCTTCAGA	TTCTCATCAT	TTTGCATCTA	TTTGTAGCC	AATAAAACTC	CGCACTAGC	

SEQ\_ID NO:18 Seq\_ID NO: 18 Protein sequence:  
 Protein Accession #: NP\_056330.1

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SGRSSPLLLG	NGKATMQNLN	DRLASYLEKV	RALEEANMKL	ESRILKWHQQ	RDPGSKKDYS	120
QYEENITHLQ	EQIVDGKMTN	AQIILLIDNA	RMAVDDFNLK	YENEHSFKKD	LEIEVEGLRR	180
TLDNLNTIVTT	DLEQEVEGMR	KELILMKEHH	EQEMEEHHVP	SDFNVNVKVD	TGPREDLIK	240
LEDMRQEYEL	I IKKKHRDLD	TWYKEQSAAM	SQEAASPATV	QSRQGDIHEL	KRTFQALEID	300
LQAQYSTKSA	LENMLSETQS	RYSKLQDMQ	EIIISHYEEEL	TQLRHELERQ	NNEYQVLLGI	360
KTHLEKEITT	YRRLLEGES	GTREESKSSM	KVSATPKIKA	ITQETINGRL	VLCQVNEIQK	420
HA						

SEQ ID NO:19 Seq ID NO: 19 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
TTTTTTTTT	TTAAAAAAA	GAGGCTTGGT	AAGTTTTGA	TACTTAGTTG	ACTTTTAGCA	60
TTATCCAGCA	TTTGATTAT	GAACCACTGA	GTACTGTAAT	TTTTCTTCC	CTTTCAGAAA	120
GACTCAAAGG	GAACATATAA	ATGTTTCCA	TTTTNNNNN	NNNNNNNNNN	NNNNNNNNNN	180
NNNNACCCAT	CGTGCATGA	TCNNNNNNN	NNNNNNNNNN	NNNNNTGGG	ATCCAGTTTC	240
AAATAAGGTA	TGGGAAAAC	AGATGTTTC	ATTATGCCA	CTTAATCCTT	ACTTCCGATT	300
ATAATTATAC	ATGTTGGCT	GTAATAACTA	TACTAAAGCA	TGCTTGTGAA	AGTAGACTTC	360
TACAAGGACA	GAAAACCCAC	AACAACAAAG	ATCGATCACG	AAAGACAAGG	CATATTCAATT	420
CATTAATTAA	CTTCTCTTAG	ACCCGGGACA	TGTGGGACAA	ATACCTTGT	CCTCATGGAT	480
GGCTTGATAA	TTTATTTATA	TGTTCTAGAG	TCTGAGGATT	TTCTTTCAGT	GGCAGACAAAC	540
AAAGGATGTT	ACAATTACT	TCAAATAAT	ACAATCATGG	TTTAATTAC	AGTGTAAATC	600
CATAACTATT	TTATAGAGAT	GGATTATCAT	ACATGGGATT	ATAAAAATAA	CTTACCCATA	660
TGCTTGAAA	ATAGACTTT	CCTATTGGG	GGAACATCTT	TTAACCTAAA	ACGGATTAT	720
TTCAGATGAA	TTAGACAGTA	CATTTTCAG	GAGAACCCAGC	CTTACTGGAT	GATCTTTGT	780
CAGGTTTGGG	GGCCTCTCT	TTGTCTTGC	AACCATAACC	CCTTTTCAGC	TGAAGACCCAC	840
TGGCCTTCAA	CCCAAGCCAG	GAGTTTGCT	CAAATGA			

SEQ ID NO:20 Seq ID NO: 20 DNA sequence

Nucleic Acid Accession #: D32051.1

Coding sequence: 72-1373

1	11	21	31	41	51	
GAATTCAAC	CAGGTGGCCA	CCCGGTGTG	GTTTCATTTT	CCTTGGAAAT	TTCTGCTTTA	60
CAGACAGAAC	AATGGCAGCC	CGAGTACTTA	TAATTGGCAG	TGGAGGAAGG	GAACATACGC	120
TGGCCTGGAA	ACTTGCACAG	TCTCATCATG	TCAAACAAAGT	GTTGGTTGCC	CCAGGAAACG	180
CAGGCACACTG	CTGCTCTGAA	AAGATTTCAA	ATACCGCCAT	CTCAATCAGT	GACCACACTG	240
CCCTTGCTCA	ATTCTGCAA	GAGAAGAAAA	TTGAATTGT	AGTTGTTGGA	CCAGAAGCAC	300
CTCTGGCTGC	TGGGATTGTT	GGGAACCTGA	GGTCTGCAGG	AGTGCAATGC	TTTGGCCCAA	360
CAGCAGAACG	GGCTCAGTTA	GAGTCCAGCA	AAAGGTTGC	CAAAGAGTTT	ATGGACAGAC	420
ATGGAATCCC	AACCGCACAA	TGGAAGGCTT	TCACCAAACC	TGAAGAAGCC	TGCAGCTTC	480
TTTGAGTGC	AGACTTCCCT	GCTTTGGTT	TGAAGGCCAG	TGGTCTTGCA	GCTGGAAAAG	540
GGGTGATTGT	TGCAAAGAGC	AAAGAAGAGG	CCTGCAAAGC	TGTACAAGAG	ATCATGCAGG	600
AGAAAGCCTT	TGGGGCAGCT	GGAGAAACAA	TTGTATTGAA	AGAACTCTT	GACGGAGAAC	660
AGGTGTCGTG	TCTGTGTTTC	ACTGATGGCA	AGACTGTGGC	CCCCATGCC	CCAGCACAGG	720
ACCATAAGCG	ATTACTGGAG	GGAGATGGT	GCCCTAACAC	AGGGGAATG	GGAGCCTATT	780
GTCCAGCCCC	TCAGGTTTCT	AATGATCTAT	TACTAAAAT	AAAGATACT	TTTCTTCAGA	840
GGACAGTGG	TGGCATGCAG	CAAGAGGGTA	CTCCATATAC	AGGTATTCTC	TATGCTGGAA	900
TAATGCTGAC	CAAGAATGGC	CCAAAAGTTC	TAGAGTTAA	TTGCCGTTT	GGTGTATCCAG	960
AGTGCCAAGT	AATCCTCCC	CTTCTAAAA	GTGATCTTA	TGAAGTGATT	CAGTCCACCT	1020
TAGATGGACT	GCTCTGCACA	TCTCTGCTG	TTGGCTAGA	AAACCACACC	GCCCTAACTG	1080
TTGTCATGGC	AAGTAAAGGT	TATCCTGGAG	ACTACACCAA	GGGTGTAGAG	ATAACAGGGT	1140
TTCCTGAGGC	TCAAGCTCTA	GGACTGGAGG	TGTCCCATGC	AGGCACGTGCC	CTCAAAAATG	1200
GCAAAGTAGT	AACTCATGGG	GGTAGAGTT	TTGCAGTCAC	AGCCATCCGG	GAAAATCTCA	1260
TATCAGCCCT	TGAGGAAGCC	AAGAAAGGAC	TAGCTGCTAT	AAAGTTTGAG	GGAGCAATT	1320
ATAGGAAAGA	CATCGGCTTT	CGTGCATAG	CTTCCCTCCA	GCAGCCCAGG	AAAAACTCTA	1380
AGCAAGTTAG	CTGTAGTGC	ATTCAGAAA	CTGGCCTAAA	TGGCTATGTA	GAACATTCCA	1440
TTAACCCCTAT	AAAGTCATTCA	GTATTCTTT	CTCTCTGTGG	GAGTGATACA	GTCTTGGTTT	1500
GTATTTTGT	TGAATCAAA	CTGGTTATAG	CAATACTCAA	ATGGAAAAAA	CTTCATGATA	1560
GCGTAAGTTT	GGAAAGTTA	GCAAATCAC	AGTGGTACTG	ATTTTATTT	GTTTTCTATT	1620
TTTTTTATTT	TATATTTTA	ATTTTTTAA	CAGGGTCTTC	CTCTCTCGCC	CAAGTTCTCA	1680
TGCCTCAGCC	TCCCCAAATAG	CTGGGACTAC	AGGCACAGGC	CACCACACCT	GGCTAATT	1740
TTTGTATTTT	TTGTGGAGAT	GGGGTTCA	ATGTTGCCAA	GGCCAGTCTG	AAAGCCTGGG	1800
CTCAAGTGT	CCTCCTGCTT	TGGCCTCCCA	AAATGCTGGG	ACTATAGGCA	TGAGGCGCTG	1860
CACTTGGCCT	GATACTGATT	TTTATTCCCT	GGCTTATCAC	ATAGTGTGTT	ATTTGAAACA	1920
TAGTTCATGG	TTTATCAAA	GAACGAAGA	TGAGAATACT	GGTCATCTAA	CTTTGTAATT	1980

TGATTTGATT ATACTGTAAA GTTTGACAGT CCCATTTAA CCTGCCTTG TATCTATTAC 2040  
TAAAATGTAT TTTTGACCT CTTACTGATT CATGGTGGT ATGTACAAAC TGTTGACTTG 2100  
TAAAATCAAT AAAGTCTTAG TTGG

SEQ ID NO:21 Seq ID NO: 21 Protein sequence:

Protein Accession #: BAA06809.1

1	11	21	31	41	51	
MAARVLIIGS	GGREHTLAWK	LAQSHHVQV	LVAPGNAGTA	CSEKISNTAI	SISDHTALAQ	60
FCKEKKIEFV	VVGPEAPLAA	GIVGNLRSAG	VQCFGPTAEA	AQLESSKRFA	KEFMDRHGIP	120
TAQWKAFTKP	EEACSFILSA	DFPALVVKAS	GLAAGKGVIV	AKSKEEACKA	VQEIMQEKAF	180
GAAGETIVIE	ELLDGEEVSC	LCFTDGKTV	PMPPAQDHKR	LLEGDGGPNT	GGMGAYCPAP	240
QVSNDLLKI	KDTVLQRTVD	GMQQEGTPYT	GILYAGIMLT	KNGPKVLEFN	CRFGDPECQV	300
ILPLLKSDLY	EVIQSTLDGL	LCTS LPVWLE	NHTALTVVMA	SKGYPGDYTK	GVEITGFPEA	360
QALGLEVSHA	GTALKNGKVV	THGGRVLAVT	AIRENLISAL	EEAKKGLAAI	KFEGAIYRKD	420
IGFRAIAFLQ	QPR					

SEQ ID NO:22 Seq ID NO: 22 DNA sequence

Nucleic Acid Accession #: EOS cloned

Coding sequence: 1-2424

1	11	21	31	41	51	
ATGCCCCCTT	TCCTGTTGCT	GGAGGCCGTC	TGTGTTTCC	TGTTTCCAG	AGTGCCCCCA	60
TCTCTCCCTC	TCCAGGAAGT	CCATGTAAGC	AAAGAAACCA	TCGGGAAGAT	TTCAGCTGCC	120
AGCAAAATGA	TGTGGTGCCTC	GGCTGCACTG	GACATCATGT	TTCTGTTAGA	TGGGTCTAAC	180
ACCGTGGGA	AAGGGAGCTT	TGAAAGGTCC	AAGCACTTG	CCATCACAGT	CTGTGACGGT	240
CTGGACATCA	GCCCCGAGAG	GGTCAGAGTG	GGAGCATTCC	AGTTCAGTTC	CACTCCTCAT	300
CTGGAATTCC	CCTTGGATTC	ATTTCAACC	CAACAGGAAG	TGAAGGCAAG	AATCAAGAGG	360
ATGGTTTCA	AAGGAGGGCG	CACGGAGACG	GAACTTGCTC	TGAAATACT	TCTGCACAGA	420
GGGTTGCCTG	GAGGCAGAAA	TGCTTCTGTG	CCCCAGATCC	TCATCATCGT	CACTGATGGG	480
AAGTCCCAGG	GGGATGTGGC	ACTGCCATCC	AAGCAGCTGA	AGGAAAGGGG	TGTCACTGTG	540
TTTGCTGTGG	GGGTCAAGGTT	TCCCAGGTGG	GAGGAGCTGC	ATGCACTGGC	CAGCGAGCCT	600
AGAGGGCAGC	ACGTGCTGTT	GGCTGAGCAG	GTGGAGGATG	CCACCAAACGG	CCTCTTCAGC	660
ACCCCTCAGCA	GCTCGGCCAT	CTGCTCCAGC	GCCACGCCAG	ACTGCAGGGT	CGAGGCTCAC	720
CCCTGTGAGC	ACAGGACGCT	GGAGATGGTC	CGGGAGTTCG	CTGGCAATGC	CCCATGCTGG	780
AGAGGATCGC	GGCGGACCCCT	TGCGGTGCTG	GCTGCACACT	GTCCTTCTA	CAGCTGGAAG	840
AGAGTGTTC	TAACCCACCC	TGCCACCTGC	TACAGGACCA	CCTGCCAGG	CCCCTGTGAC	900
TCGCAGCCCT	GCCAGAATGG	AGGCACATGT	GTTCCAGAAG	GAUTGGACGG	CTACCACTG	960
CTCTGCCCGC	TGGCCTTGG	AGGGGAGGCT	AACTGTGCC	TGAAGCTGAG	CCTGGAATGC	1020
AGGGTCGACC	TCCTCTTCCT	GCTGGACAGC	TCTGCGGGCA	CCACTCTGGA	CGGCTTCCTG	1080
CGGGCCAAG	TCTTCGTGAA	CGGGTTTGTG	CGGGCCGTGC	TGAGCGAGGA	CTCTCGGGCC	1140
CGAGTGGGTG	TGCCACATA	CAGCAGGGAG	CTGCTGGTGG	CGGTGCCTGT	GGGGGAGTAC	1200
CAGGATGTGC	CTGACCTGGT	CTGGAGCCTC	GATGGCATT	CCTTCCGTGG	TGGCCCCACC	1260
CTGACGGGCA	GTGCCCTGCG	GCAGCGGCA	GAGCGTGGCT	TCGGGAGCGC	CACCAAGGACA	1320
GGCCAGGACC	GGCCACGTAG	AGTGGTGGTT	TTGCTCACTG	AGTCACACTC	CGAGGATGAG	1380
GTTGCGGGCC	CAGCGCGTC	CGCAAGGGCG	CGAGAGCTGC	TCCTGCTGGG	TGTAGGCAGT	1440
GAGGCCGTGC	GGGCAGAGCT	GGAGGAGATC	ACAGGCAGCC	CAAAGCATGT	GATGGTCTAC	1500
TCGGATCCTC	AGGATCTGTT	CAACCAAATC	CCTGAGCTGC	AGGGGAAGCT	GTGCAGCCGG	1560
CAGCGGCCAG	GGTGCCGGAC	ACAAGCCCTG	GACCTCGTCT	TCATGTTGGA	CACCTCTGCC	1620
TCAGTAGGGC	CCGAGAATT	TGCTCAGATG	CAGAGCTTG	TGAGAAAGCTG	TGCCCTCCAG	1680
TTTGAGGTGA	ACCCGTACGT	GACACAGGTC	GGCCTGGTGG	TGTATGGCAG	CCAGGTGCGAG	1740
ACTGCCCTCG	GGCTGGACAC	CAAACCCACC	CGGGCTGCAG	TGCTGCGGGC	CATTAGCCAG	1800
GCCCCCTAAC	TAGGTGGGGT	GGGCTCAGCC	GGCACCGCCC	TGCTGCACAT	CTATGACAAA	1860
GTGATGACCG	TCCAGAGGGG	TGCCCCGGCCT	GGTGTCCCCA	AAGCTGTGGT	GGTGCTCAC	1920
GGCGGGAGAG	GCGCAGAGGA	TGCAGCGT	CCTGCCAGA	AGCTGAGGAA	CAATGGCAGTC	1980
TCTGTCTTGG	TCGTTGGCGT	GGGGCCTGTC	CTAAGTGGAG	GTCTGCGGAG	GCTTGCAGGT	2040
CCCCGGGATT	CCCTGATCCA	CGTGGCAGCT	TACGCCGACC	TGCGGTACCA	CCAGGACGTG	2100

CTCATTGAGT GGCTGTGTGG AGAACCAAG CAGCCAGTCA ACCTCTGC<sub>AA</sub> ACCCAGCCG 2160  
 TGCATGAATG AGGGCAGCTG CGTCCTGCAG AATGGGAGCT ACCGCTGC<sub>AA</sub> GTGTGGGAT 2220  
 GGCTGGGAGG GCCCCCACTG CGAGAACCGT GAGTGGAGCT CTTGCTCTGT ATGTGTGAGC 2280  
 CAGGGATGGA TTCTTGAGAC GCCCCTGAGG CACATGGCTC CCGTGCAGGA GGGCAGCAGC 2340  
 CGTACCCCTC CCAGCAACTA CAGAGAAGGC CTGGGCACTG AAATGGTGCC TACCTTCTGG 2400  
 AATGTCTGTG CCCCAGGTCC TTAG

SEQ ID NO:23 Seq ID NO: 23 Protein sequence:

Protein Accession #: EOS cloned

1	11	21	31	41	51	
MPPFLLLEAV	CVFLFSRVPP	SLPLQEVIHVS	KETIGKISAA	SKMMWCSAAV	DIMFLLDGSN	60
SVKGKSFERS	KHFAITVCVG	LDISPERVRV	GAQFQSSTPH	LEFPLDSFST	QQEVKARIKR	120
MVFKGGRTE	ELALKYLLHR	GLPGGRNASV	PQILIIVTDG	KSQGDVALPS	KQLKERGVTV	180
FAVGVRFPRW	EELHALASEP	RQHQVLLAEQ	VEDATNGLFS	TLSSSAICSS	ATPDCRVEAH	240
PCEHRTLEMV	REFAGNAPCW	RGSRRTLAVL	AAHCPFYSWK	RVFLTHPATC	YRTTCPGPCD	300
SQPCQNGGTC	VPEGLDGYQC	LCPLAFGGEA	NCALKLSLEC	RVDLLFLLDS	SAGTTLDGFL	360
RAKVFVKRFV	RAVLSEDSRA	RVGVATYSRE	LLVAVPVGEY	QDVPDLVWSL	DGIPFRGGPT	420
LTGSALRQAA	ERGFGSATRT	GQDRPRRRVVV	LLTESHSEDE	VAGPARHARA	RELLLLGVGS	480
EAVRAELEEI	TGSPKHVMVY	SDPQDLFNQI	PELQGKLCsr	QRPGCRTQAL	DLVFMLDTS	540
SVGPNENFAQM	QSFVRSCALQ	FEVNPDVTQV	GLVVYGSQVQ	TAFGLDTKPT	RAAMLRAISQ	600
APYLGGVGSA	GTALLHIYDK	VMTVQRGARP	GVPKAVVVLT	GGRGAEDAAB	PAQKLRNNGI	660
SVLVVGVPV	LSEGILRRLAG	PRDSLIVHAA	YADLRYHQDV	LIEWLCEAK	QPVNLCKPSP	720
CNEGSCV	NGSYRCKRD	GWEGPHCENR	EWSSCSVCVS	QGWILETPLR	HMAPVQEGSS	780
RTPPSNYREG	LGTEMVPTFW	NVCAPGP				

SEQ ID NO:24 Seq ID NO: 24 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
AGGTCGGCTG	GTTATCGGGG	GTTGGAGGGC	TGAGGTCGGG	AGGGTGGTGT	GTACAGAGCT	60
CTAGGACTCA	CGCACCCAGGC	CAGTCGGGG	TTTGGGCCG	AGGCCTGGGT	TACAAGCAGC	120
AAGTGGCGGG	TTGGGGCCAC	TGCGAGGGCG	TTTAGAAAA	CTGTTAAAA	CAAAGAGCAA	180
TTGATGGATA	AATCAGGAAT	AGATTCTCTT	GACCATGTGA	CATCTGATGC	TGTGGAACCTT	240
GCAAATCGAA	GTGATAACTC	TTCTGATAGC	AGCTTATT	AAACTCAGTG	TATCCCTTAC	300
TCACCTAAAG	GGGAGAAAAG	AAACCCATT	CGAAAATTG	TTCTACACC	TGAAAGTGT	360
CACGCAAGTA	TTCATCAAGT	GACTCATCTT	TTGAACCACT	ACCATTGACT	ATAAAAGCTA	420
TTTTGAAAG	ATTCAAGAAC	AGGAAAAAGA	GATATAAAA	AAAGAAAAG	AGGAGGTACC	480
AGCCAACAGG	AAGACCACGG	GGAAAGACAG	AAGGAAGGAG	AAATCCTATA	TACTCACTAA	540
TAGATAAGAA	GAAACAATT	AGAACGAG	GATCTGGCTT	CCCATT	GAATCAGAGA	600
ATGAAAAAAA	CGCACCTTGG	AGAAAATT	TAACGTTGA	GCAAGCTGTT	GCAAGAGGAT	660
TTTTTAAC	TATTGAAAAA	CTGAAGTATG	AAACACCAC	GAAAGAATCA	TTGAAGCAAA	720
TGAATGTTGG	TGAAGATT	GAAAATGAAG	ATTTGACAG	TCGTAGATAC	AAATTTTG	780
ATGATGATGG	ATCCATT	CCTATTGAGG	AGTCAACGCT	TTTATCTTGA	GGACATGGTG	840
TCTGGAGTTA	AAGGTATTGG	CATACTCCAC	ACATCTGTAC	CATTCTTGAG	TGATCGCTTA	900
GGAATGAATG	TGATTTGGAC	TCATTCTATG	ATGAGAGTAA	GCAATGCTT	TTTTCCAGG	960
GTGTCAAATT	GAGAACCGAG	TAGATCCCCA	CCACCTACAG	AAAAAGGAC	CCTAAAGTAA	1020
ATTGGTTGAA	GAAATTAGAT	CCCAAAGATT	CTTGGTGAAT	TTTGAAGTCT	TCATCAGTAT	1080
ATCCATATTA	AAACGGAGATG	ACAGAACCA	AAGTAATTAT	GGGCTGACAG	GACAAC	1140
TCAGTTTCA	AAAAAGGGC	AAACTTGAAG	ATAAATCTT	TGACTCCAGC	TCTTAGAGG	1200
ATCTAAAGTG	ACCTTGATGG	ACAGTGGAAAG	AAATCACAAAC	ATGGAATTCC	TCGAATAACA	1260
ATTATTGAC	TTTAAATAAT	TTTGTCTAAT	GCTACATATA	CACAATTAAA	AAACCTTAC	1320
ACTATTCTA	GAAAGTCAGC	ATGTATT	GGCTCGAAGT	TTCTCTAGTG	TTTCTGTGG	1380
AAGGAATAAA	AATTGAGGT	TTCAATACAA	AAACAAAACA	AACAACACGA	AACACGAAA	1440
ACAATCTGTT	GTGCGGCGCC	CCTGGGCC	TTGAGAGAAA	ACTTTT	ACCCCTTTG	1500
CGTTGTGGCG	GCCCCGGGGC	CCCACAGTTG	GGTTTAGGTG	GGCACCC	TGTCTACAAG	1560
TGGTGTCTCC	CCAAGAGAGA	GAACACCTCC	GGGGTCAAGC	GGACAACAAG	AGTGC	1620

GAGGACTCTT CACCCAAAGT ATATAAAACC CGCCCCGC GGAAACCACC GGCGCTTT 1680  
 CTGTAGACAC AACCCCCACA GTGGGAACCT CTGAGGGCGC ACACACAGGG CGAGCCTTAT 1740  
 CAACAAGGGG TGCCCAACAG AAACCCCGAG TTAAAAATCG

SEQ ID NO:25 Seq ID NO: 25 DNA sequence  
 Nucleic Acid Accession #: BC001972.1  
 Coding sequence: 183-1019

1	11	21	31	41	51	
GGTCGGCTGG	TTATCGGGAG	TTGGAGGGCT	GAGGTGGGA	GGGTGGTGTG	TACAGAGCTC	60
TAGGACTCAC	GCACCAGGCC	AGTCGCGGT	TTGGGCCGA	GGCCTGGT	ACAAGCAGCA	120
AGTGCAGGGT	TGGGCCACT	GCGAGGCCGT	TTTAGAAAAC	TGTTTAAAC	AAAGAGCAAT	180
TGATGGATAA	ATCAGGAATA	GATTCTCTG	ACCATGTGAC	ATCTGATGCT	GTGGAACCTG	240
CAAATCGAAG	TGATAACTCT	TCTGATAGCA	GCTTATTTAA	AACTCAGTGT	ATCCCTTA	300
CACCTAAAGG	GGAGAAAAGA	AACCCCATT	AAAAATTGT	TCGTACACCT	GAAAGTGTTC	360
ACGCAAGTGA	TTCATCAAGT	GACTCATCTT	TTGAACCAAT	ACCATTGACT	ATAAAAGCTA	420
TTTTTGAAG	ATTCAAGAAC	AGGAAAAGA	GATATAAAA	AAAGAAAAG	AGGAGGTACC	480
AGCCAACAGG	AAGACCACGG	GGAAGACCG	AAGGAAGGAG	AAATCCTATA	TACTCACTAA	540
TAGATAAGAA	GAAACAATT	AGAACAGAG	GATCTGGCTT	CCCATTTTA	GAATCAGAGA	600
ATGAAAAAAA	CGCACCTTG	AGAAAAATT	TAACGTTGA	GCAAGCTGTT	GCAAGAGGAT	660
TTTTTAAC	TATTGAAAAA	CTGAAGTATG	AACACCACCT	GAAAGAATCA	TTGAAGCAAA	720
TGAATGTTGG	TGAAGATT	GAAAATGAAG	ATTTGACAG	TCGTAGATAC	AAATTTTG	780
ATGATGATGG	ATCCATT	CCTATTGAGG	AGTCAACAGC	AGAGGATGAG	GATGCAACAC	840
ATCTTGAAGA	TAACCAATGT	GATATCAAAT	TGGCAGGGGA	TAGTTCATA	GTAAGTTCTG	900
AATTCCCTGT	AAGACTGAGT	GTATACTTAG	AAGAACAGGA	TATTACTGAA	GAAGCTGCTT	960
TGTCTAAAAA	GAGAGCTACA	AAAGCCAAA	ATACTGGACA	GAGAGGCC	AAAATGTGAC	1020
AGGATCATGA	ATGTCAAAGG	CTTTATCTT	GAGAACATGG	TGTCTGGAGT	TAAGGACTA	1080
TTGTTAGATC	TGTGGGAAGG	AATTACAAGA	CAGTGCTAA	AAGTTGAAA	AAGACGGTTG	1140
CTAACACGTTA	TGAAAAACCA	GATAATCTAC	TTTTTACCT	TAGGTATTGG	CATACTCCAC	1200
ACATCTGTAC	CATTCTTGAG	TGATCGCTT	GGAATGAATG	TGATTGAAAC	TCATTGATGT	1260
TGAGAGGGTG	TCAAATTGAG	AACCAGGTAG	ATCCCCACCA	CCTACAGTAA	AAAGGACCT	1320
AAAGTAAATT	GGTTGAAGAA	ATTAGATCCC	AAAGATTCTT	GGTGAATT	GAAGTCTTCA	1380
TCAGTATATC	CATATTAAA	CGAGATGACA	GAAGCCAAAG	TAATTATGGG	CTGACAGGAC	1440
AACTGGATCA	GTTTCATTAA	AAAGGGCAA	CTTGAAGATA	AATCTTTGA	CTCCAGCTCT	1500
TTAGAGGATC	TAAAGTGACC	TTGATGGACA	GTGGAAGAAA	TCACAAACATG	GAATTCTCG	1560
AATAACAATT	TATTGACTT	AAATAATT	GTCTAATGCT	ACATATACAC	AATTAAAAAA	1620
CCTTTACACT	AAAAAA	AAAAAA				

SEQ ID NO:26 Seq ID NO: 26 Protein sequence:  
 Protein Accession #: AAH01972.1

1	11	21	31	41	51	
MDKSGIDS	HVTSDAVELA	NRSNDSSDSS	LFKTQCIPYS	PKGEKRNP	KFVRTPESVH	60
ASDSSSDSSF	EPIPLTIKAI	FERFKNRKKR	YKKKKRRYQ	PTGRPRGRPE	GRRNPIYSLI	120
DKKKQFRSRG	SGFPFLESEN	EKNAPWRKIL	TFEQAVARGF	FNYIEKLKYE	HHLKESLKQM	180
NVGEDLENED	FDSRRYKFLD	DDGSISPIEE	STAEDEDATH	LEDNECDIKL	AGDSFIVSSE	240
FPVRLSVYLE	EEDITEEAL	SKKRATKAKN	TGQRGLKM			

SEQ ID NO:27 Seq ID NO: 27 DNA sequence  
 Nucleic Acid Accession #: AK027016  
 Coding sequence: 207-1043

1	11	21	31	41	51	
CTTTTCTTCC	GCACGGTTGG	AGGAGGTCGG	CTGGTTATCG	GGAGTTGGAG	GGCTGAGGTC	60
GGGAGGGTGG	TGTGTACAGA	GCTCTAGGAC	TCACGCACCA	GGCCAGTCGC	GGATTTGGG	120

CCGAGGCCTG	GGTTACAAGC	AGCAAGTGC	CGGTTGGGGC	CACTGCGAGG	CCGTTTTAGA	180
AAACTGTTA	AAACAAAGAG	CAATTGATGG	ATAAATCAGG	AATAGATTCT	CTTGACCATG	240
TGACATCTGA	TGCTGTGGAA	CTTGCAAATC	GAAGTGATAA	CTCTTCTGAT	AGCAGCTTAT	300
TTAAAACCTCA	GTGTATCCCT	TACTCACCTA	AAGGGGAGAA	AAGAAACCCC	ATTCGAAAAT	360
TTGTTCGTAC	ACCTGAAAGT	GTTCACGCCA	GTGATTCATC	AAGTGACTCA	TCTTTGAAC	420
CAATACCAT	GACTATAAAA	GCTATTTTG	AAAGATTCAA	GAACAGGAAA	AAGAGATATA	480
AAAAAAAGAA	AAAGAGGAGG	TACCAGCCAA	CAGGAAGACC	ACGGGGAAAGA	CCAGAAGGAA	540
GGAGAAATCC	TATATACTCA	CTAATAGATA	AGAAGAAACA	ATTTAGAACG	AGAGGATCTG	600
GCTTCCCATT	TTTAGAATCA	GAGAATGAAA	AAAACGCACC	TTGGAGAAAA	ATTTAACGT	660
TTGAGCAAGC	TGTTGCAAGA	GGATTTTTA	ACTATATTGA	AAAGCTGAAG	TATGAACACC	720
ACCTGAAAGA	ATCATTGAAG	CAAATGAATG	TTGGTGAAGA	TTTAGAAAAT	GAAGATTTG	780
ACAGTCGTAG	ATACAAATT	TTGGATGATG	ATGGATCCAT	TTCTCCTATT	GAGGAGTCAA	840
CAGCAGAGGA	TGAGGATGCA	ACACATCTG	AAGATAACGA	ATGTGATATC	AAATTGGCAG	900
GGGATAGTT	CATAGTAAGT	TCTGAATTCC	CTGTAAGACT	GAGTGTATAC	TTAGAAGAAG	960
AGGATATTAC	TGAAGAAGCT	GCTTTGCTA	AAAAGAGAGC	TACAAAAGCC	AAAATACTG	1020
GACAGAGAGG	CCTGAAATG	TGACAGGATC	ATGAATGTCA	AAGGCTTTA	TCTTGAGAAC	1080
ATGGTGTCTG	GAGTTAAAGG	TATTGGCATA	CTCCACACAT	CTGTACCATT	CTTGAGTGAT	1140
CGCTTAGGAA	TGAATGTGAT	TTGAACTCAT	TCATGTTGAG	AGGGTGTCAA	ATTGAGAACCC	1200
AGGTAGATCC	CCACCACTA	CACTAAAAAG	GACCCCTAAAG	TAAATTGGTT	GAAGAAATT	1260
GATCCCAAAG	ATTCTTGGTG	AATTTTGAAG	TCTTCATCAG	TATATCCATA	TTAAAACGAG	1320
ATGACAGAAG	CCAAAGTAAT	TATGGCAAGT	AATGGTTTTT	ATCTTAACTA	TAAGTTATT	1380
GCTCAAGGGT	GTAATGGTCA	TTACCAAGGC	TTTTAGAATG	CAGTTCTCA	TTTGCTGTGG	1440
ACATGACCAT	AAAAAAAAT	TTCCCACTAG	GTTCCTATC	TGCTACGTTG	CTAGCAATCA	1500
GCTTATTGGG	AACAGTTGAT	TAACTGTAAT	AGAAAATGCAA	TACAAATAAA	ATGTGAACCA	1560
CATGTGATT	TTCTTAAAAA	TCAGTGAGAT	TTGAAAATTC	TCCTAGATCT	CTTGAAATCAT	1620
GCAAATTGTC	TTTGCCTTA	TATTGTAACC	CTTGTGGGTT	GCTAATAACC	AAGCAGTTTG	1680
TAGTAGAGTT	AACTCAGGCT	CGTTCTAGGG	ACTCATTATC	GTTCACTCAC	TGTACACTCA	1740
TCTCTGGAAA	TGTAAAATT	ACTTTTATAC	TATTGTTATG	TAGGGCTGAC	AGGACAAC	1800
GATCAGTTTC	ATTAAAAAGG	TATGTATGCA	TTAGAAAAGA	CATTGTATG	GGTCATTTCA	1860
AAGAGGGCTT	ATGAGGCTGT	GAAACCCAGA	GCTCTTAACG	CTGTGACCAA	AGATGGAAGT	1920
TCTCTATAGG	AAGCCATAGC	ACTCCTAATG	TTTGGTGCTA	TGTTTCCTG	AGGAGATATA	1980
AAACGTAATA	ATCCATGATT	GTTGCCATGT	GAGAGTTTA	AAGGTTAAC	AAAATTCTC	2040
TTCTTCAGGG	CAAACCTGAA	GATAAACTT	TTGACTCCAG	CTCTTAGAG	GATCTAAAGT	2100
GACCTTGATG	GACAGTGGAA	GAAATCACAA	CATGGAATTC	CTCGAATAAC	AATTATTGTA	2160
CTTTAAATAA	TTTTGTCTAA	TGCTACATAT	ACACAATTAA	AAAACCTTA	CACTATTCT	2220
AGAAAGTCAG	CATGTATT	TGGCTCGAAG	TTCTCTAGT	GTTCCTGTG	GAAGGAATAA	2280
AAATTGAGT	TTCAAAAAAA	AAAAAAA	AAAAAAA	AAAAAAA	AAAAAA	

SEQ ID NO:28 Seq ID NO: 28 Protein sequence:

Protein Accession #: BAB15628.1

1	11	21	31	41	51	
MDKSGIDS	LD HVTSDAVELA	NRSDNSSDSS	LFKTQCIPYS	PKGEKRNP	KFVRTPESVH	60
ASDSSSDSSF	EPIPLTIKAI	FERFKNRKKR	YKKKKKRRYQ	PTGRPRGRPE	GRRNPIYSLI	120
DKKKQFRSRG	SGFPFLESEN	EKNAPWRKIL	TFEQAVALGF	FNYIEKLKYE	HHLKESLKQM	180
NVGEDLENED	FDSRRYKFLD	DDGSISPIEE	STAEDEDATH	LEDNECDI	KL AGDSFIVSSE	240
FPVRLSVYLE	EEDITEEAL	SKKRATKAKN	TGQRGLKM			

SEQ ID NO:29 Seq ID NO: 29 DNA sequence

Nucleic Acid Accession #: NM\_004289.3

Coding sequence: 493-1695

1	11	21	31	41	51	
GCCGCCGCCT	CGTCCACCGG	AGGAGCCGGC	GCCAGCGTGG	ACGGCGGCAG	CCAGGCTGTG	60
CAGGGGGCG	GCAGGGACCC	CCGAGCGGCT	CGGAGTGGCC	CCTTGGACGC	CGGGGAAGAG	120
GAGAAGGCAC	CCGCGGAACC	GACGGCTCAG	GTGCCGGACG	CTGGCGGATG	TGCGAGCGAG	180
GAGAATGGGG	TACTAAGAGA	AAAGCACGAA	GCTGTGGATC	ATAGTCCCA	GCATGAGGAA	240

AATGAAGAAA	GGGTGTCAGC	CCAGAAGGAG	AACTCACTTC	AGCAGAACATGA	TGATGATGAA	300
AACAAAATAG	CAGAGAAACC	TGACTGGGAG	GCAGAAAAAGA	CCACTGAATC	TAGAAATGAG	360
AGACATCTGA	ATGGGACAGA	TACTTCTTC	TCTCTGGAAG	ACTTATTCCA	GTTGCTTC	420
TCACAGCCTG	AAAATTCACT	GGAGGGCATC	TCATTGGGAG	ATATTCCCT	TCCAGGCAGT	480
ATCAGTGATG	GCATGAATTC	TTCAGCACAT	TATCATGTAA	ACTTCAGCCA	GGCTATAAGT	540
CAGGATGTGA	ATCTTCATGA	GGCCATCTTG	CTTGTCCCCA	ACAATACATT	TAGAAGAGAT	600
CCAACAGCAA	GGACTTCACA	GTCACAAAGAA	CCATTTCTGC	AGTTAAATTC	TCATACCAACC	660
AATCCTGAGC	AAACCCCTCC	TGGAACTAAT	TTGACAGGAT	TTCTTCACC	GGTTGACAAT	720
CATATGAGGA	ATCTAACAAAG	CCAAGACCTA	CTGTATGACC	TTGACATAAA	TATATTTGAT	780
GAGATAAACT	TAATGTCATT	GGCCACAGAA	GACAACTTTG	ATCCAATCGA	TGTTTCTCAG	840
CTTTTGATG	AACCAGATT	TGATTCTGGC	CTTCTTTAG	ATTCAAGTCA	CAATAATACC	900
TCTGTCATCA	AGTCTAATT	CTCTCACTCT	GTGTGTGATG	AAGGTGCTAT	AGGTTATTGC	960
ACTGACCAGT	AATCTAGTT	CCATCATGAC	TTAGAAGGTG	CTGTAGGTGG	CTACTACCCA	1020
GAACCCAGTA	AGCTTTGTCA	CTTGGATCAA	AGTGATTCTG	ATTTCCATGG	AGATCTTACA	1080
TTTCAACACG	TATTCATAA	CCACACTTAC	CACTTACAGC	CAACTGCACC	AGAATCTACT	1140
TCTGAACCTT	TTCCGTGGCC	TGGGAAGTCA	CAGAAGATAA	GGAGTAGATA	CCTTGAAGAC	1200
ACAGATAGAA	ACTTGAGCCG	TGATGAACAG	CGTGCTAAAG	CTTGCATAT	CCCTTTTCT	1260
GTAGATGAAA	TTGTCGGCAT	GCCTGTTGAT	TCTTCAATA	GCATGTTAAG	TAGATATTAT	1320
CTGACAGACC	TACAAGTCTC	ACTTATCCGT	GACATCAGAC	GAAGAGGGAA	AAATAAAGTT	1380
GCTGCGCAGA	ACTGTCGTA	ACGCAAATTG	GACATAATT	TGAATTAGA	AGATGATGTA	1440
TGTAACCTGC	AAGCAAAGAA	GGAAACTCTT	AAGAGAGAGC	AAGCACAATG	TAACAAAGCT	1500
ATTAACATAA	TGAAACAGAA	ACTGCATGAC	CTTATCATG	ATATTTTAG	TAGATTAAGA	1560
GATGACCAAG	GTAGGCCAGT	CAATCCCAAC	CACTATGCTC	TCCAGTGTAC	CCATGATGGA	1620
AGTATCTGA	TAGTACCCAA	AGAACTGGT	GCCTCAGGCC	ACAAAAAGGA	AACCCAAAAG	1680
GGAAAGAGAA	AGTGAGAAGA	AACTGAAGAT	GGACTCTATT	ATGTGAAGTA	GTAATGTTCA	1740
GAAACTGATT	ATTTGGATCA	GAAACCATTG	AAACTGCTTC	AAGAATTGTA	TCTTTAAGTA	1800
CTGCTACTTG	AATAACTCA	TTAACGCTGT	TTTGAAGCTT	ACATGGACAA	ATGTTTAGGA	1860
CTTCAAGATC	ACACTTGTGG	GCAATCTGGG	GGAGGCCACAA	CTTTCATGA	AGTGCATTGT	1920
ATACAAAATT	CATAGTTATG	TCCAAAGAAT	AGGTTAACAT	GAAAACCCAG	TAAGACTTTC	1980
CATCTGGCA	GCCATCCTT	TTAAGAGTAA	GTTGGTTACT	TCAAAAAGAG	CAAACACTGG	2040
GGATCAAATT	ATTTTAAGAG	GTATTTCACT	TTTAAATGCA	AAATAGCCTT	ATTTTCATT	2100
AGTTTGTAG	CACTATAGTG	AGCTTTCAA	ACACTATT	AATCTTATA	TTTAACATT	2160
AAATTTTGCT	TTCT					

SEQ ID NO:30 Seq ID NO: 30 Protein sequence:

Protein Accession #: NP\_004280

1	11	21	31	41	51	
MNSSAHYHVN	FSQAIISQDVN	LHEAILLCPN	NTFRRDPTAR	TSQSQEPLQ	LNSHTTNPEQ	60
TLPGTNLTGF	LSPVDNHMRN	LTSQDLLYDL	DINIFDEINL	MSLATEDNFD	PIDVSQLFDE	120
PDSDSGLSLD	SSHNNNTSVIK	SNSSHSVCDE	GAIGYCTDHE	SSSHHDLEGA	VGGYYPEPSK	180
LCHLDQSDSD	FHGDLTFQHV	FHNHTYHLQP	TAPESTSEPF	PWPGKSQKIR	SRYLEDTDRN	240
LSRDEQRAKA	LHIPFSVDEI	VGMPVDSFNS	MLSRYYLTDL	QVSLIRDIRR	RGKNKVAQN	300
CRKRKLDIIL	NLEDDVCNLQ	AKKETLKREQ	AQCNKAINIM	KQKLHDLYHD	IFSRLRDDQG	360
RPVNPNHYAL	QCTHDGSIL	VPKELVASGH	KKETQKGKRK			

SEQ ID NO:31 Seq ID NO: 31 DNA sequence

Nucleic Acid Accession #: NM\_033260.1

Coding sequence: 1-1208

1	11	21	31	41	51	
ATGAAGTTGG	AGGTGTTCGT	CCCTCGCGCG	GCCCCACGGGG	ACAAGCAGGG	CAGTGACCTG	60
GAGGGCGCGG	GCAGGCAGCGA	CGCGCCGTCC	CCGCTGTCGG	CGGCGGGAGA	CGACTCCCTG	120
GGCTCAGATG	GGGACTGCGC	GGCCAAGCCG	TCCGCGGGCG	GCAGGCCAG	AGATACGCAG	180
GGCGACGGCG	AACAGAGTGC	GGGAGGGCGG	CCGGGCGCGG	AGGAGGCGAT	CCCAGCAGCA	240
GCTGCTGCGAG	CGGTGGTGGC	GGAGGGCGCG	GAGGGCGGGG	CGGCGGGGCC	AGGCGCGGGC	300
GGCGCGGGGA	GCAGGCAGGG	TGCACGCAGC	AAGCCATATA	CGCGGCGGCC	CAAGCCCCCC	360

TACTCGTACA	TCGCGCTCAT	CGCCATGGCC	ATCCGCGACT	CGGCGGGCGG	GCGCTTGACG	420
CTGGGGAGA	TCAACGAGTA	CCTCATGGC	AAGTTCCCCT	TTTCCCGGG	CAGCTACACG	480
GGCTGGCGA	ACTCCGTGCG	CCACAACCTT	TCGCTCAACG	ACTGCTTCGT	CAAGGTGCTG	540
CGCGACCCT	CGCGGCCCTG	GGGCAAGGAC	AACTACTGGA	TGCTCAACCC	CAACAGCGAG	600
TACACCTTCG	CCGACGGGGT	CTTCCGCGCG	CGCCGCAAGC	GCCTCAGCCA	CCGCGCGCCG	660
GTCCCCGCGC	CCGGGCTGCG	GCCCAGGAG	GCCCCGGGCG	TCCCCGCCG	CCCGCGGCC	720
GCGCCCGCCG	CCCCGGCCTC	GCCCCGCATG	CGCTCGCCCG	CCCGCCAGGA	GGAGCGCGCC	780
AGCCCCGCGG	GCAAGTTCTC	CAGCTCCCTC	GCCATCGACA	GCATCTGCG	CAAGCCCTTC	840
CGCAGCCGTC	GCCTCAGGGA	CACGGCCCCC	GGGACGACGC	TTCAGTGGGG	CGCCGCGCCC	900
TGCCCGCCGC	TGCCCCGCGTT	CCCCGCGCTC	CTCCCCGCGG	CGCCCTGCAG	GGCCCTGCTG	960
CCGCTCTGGG	CGTACGGCGC	GGGCGAGCCG	GCGCGGCTGG	GCGCGCGCGA	GGCCGAGGTG	1020
CCACCGACCG	CGCCGCCCCCT	CCTGCTTGCA	CCTCTCCCGG	CGGCGGCC	CGCCAAGCCA	1080
CTCCGAGGCC	CGGCGGCCGG	CGGCGCGCAC	CTGTACTGCC	CCCTGCGGCT	GCCCGCAGCC	1140
CTGCAGGCCG	CCTTAGTCCG	NCGTCTGGC	CCGCACCTGT	CGTACCCGGT	GGAGACGCTC	1200
CTAGCTTGA						

SEQ ID NO:32 Seq ID NO: 32 Protein sequence:

Protein Accession #: NP\_150285.1

1	11	21	31	41	51	
MKLEVFPRA	AHGDKQGSDL	EGAGGSDAPS	PLSAAGDDSL	GSDGDCAAkp	SAGGGARDTQ	60
GDGEQSAGGG	PGAEAAIPAA	AAAAVVAEGA	EAGAAAGPGAG	GAGSGEGARS	KPYTRRPKPP	120
YSYIALIAMA	IRDSAGGRLT	LAEINEYLMG	KPFFFRGSYT	GWRNSVRHNL	SLNDCFVKVL	180
RDPSRPWGKD	NYWMLNPNSE	YTFADGVFRR	RRKRLSHRAP	VPAPGLRPEE	APGLPAAPPP	240
APAAPASPRM	RSPARQEERA	SPAGKFSSSF	AIDSILRKPF	RSRRLRDTAP	GTTLQWGAAP	300
CPPLPAFPAL	LPAAPCRALL	PLCAYGAGEP	ARLGAREAEV	PPTAPPPLLA	PLPAAAPAKP	360
LRGPAAGGAH	LYCPLRLPAA	LQAALVRRPG	PHLSYPVETL	LA		

SEQ ID NO:33 Seq ID NO: 33 DNA sequence

Nucleic Acid Accession #: NM\_012128.2

Coding sequence: 43-2796

1	11	21	31	41	51	
GAACAAACCA	ACATTGAGC	CAGGAATAAC	TAGAGAGGAA	CAATGGGTT	ATTCAGAGGT	60
TTGTTTTCC	TCTTAGTTCT	GTGCCTGCTG	CACCAAGTAA	ATACTTCCTT	CATTAAGCTG	120
AATAATAATG	GCTTGAAGA	TATTGTCATT	GTTATAGATC	CTAGTGTGCC	AGAAGATGAA	180
AAAATAATTG	AACAAATAGA	GGATATGGTG	ACTACAGCTT	CTACGTACCT	GTTTGAAGCC	240
ACAGAAAAAA	GATTTTTTTT	CAAAAATGTA	TCTATATTAA	TTCCTGAGAA	TTGGAAGGAA	300
AATCCTCACT	ACAAAAGGCC	AAAACATGAA	AACCATAAAC	ATGCTGATGT	TATAGTTGCA	360
CCACCTACAC	TCCCAGGTAG	AGATGAACCA	TACACCAAGC	AGTTCACAGA	ATGTGGAGAG	420
AAAGGCGAAT	ACATTCACTT	CACCCCTGAC	CTTCTACTTG	GAAAAAAACA	AAATGAATAT	480
GGACCACCA	GCAAACGT	TGTCCATGAG	TGGGCTCACC	TCCGGTGGGG	AGTGTGTTGAT	540
GAGTACAATG	AAGATCAGCC	TTTCTACCGT	GCTAAGTCAA	AAAAAAATCGA	ACCAACAAGG	600
TGTTCCGCG	GTATCTCTGG	TAGAAATAGA	GTTTATAAGT	GTCAAGGAGG	CAGCTGTCTT	660
AGTAGAGCAT	GCAGAATTGA	TTCTACAACA	AAACTGTATG	GAAAAGATTG	TCAATTCTTT	720
CCTGATAAAAG	TACAAACAGA	AAAAGCATCC	ATAATGTTA	TGCAAAGTAT	TGATTCTGTT	780
GTTGAATT	GTAACGAAA	AAACCCATAAT	CAAGAAGCTC	CAAGCCTACA	AAACATAAAAG	840
TGCAATT	GAAGTACATG	GGAGGTGATT	AGCAATTCTG	AGGATTTTAA	AAACACCATA	900
CCCATGGTGA	CACCAACCTCC	TCCACCTGTC	TTCTCATTGC	TGAAGATCCG	TCAAAGAATT	960
GTGTGCTTAG	TTCTTGATAA	GTCTGGAAGC	ATGGGGGGTA	AGGACCGCCT	AAATCGAATG	1020
AATCAAGCAG	CAAAACATT	CCTGCTGCG	ACTGTTGAAA	ATGGATCCTG	GGTGGGGATG	1080
GTTCACT	ATAGTACTGC	CACTATTGTA	AATAAGCTAA	TCCAAATAAA	AAGCAGTGAT	1140
GAAAGAAACA	CACTCATGGC	AGGATTACCT	ACATATCCTC	TGGGAGGAAC	TTCCATCTGC	1200
TCTGGAATT	AATATGCATT	TCAGGTGATT	GGAGAGCTAC	ATTCCCAACT	CGATGGATCC	1260
GAAGTACTGC	TGCTGACTGA	TGGGGAGGAT	AACACTGCAA	GTTCTTGTAT	TGATGAAGTG	1320
AAACAAAGTG	GGGCCATTGT	TCATTTATT	GCTTGGGAA	GAGCTGCTGA	TGAAGCAGTA	1380
ATAGAGATGA	GCAAGATAAC	AGGAGGAAGT	CATTTTATG	TTTCAGATGA	AGCTCAGAAC	1440

AATGGCCTCA TTGATGCTTT TGGGGCTCTT ACATCAGGAA ATACTGATCT CTCCCAGAACG 1500  
TCCCTTCAGC TCGAAAGTAA GGGATTAAACA CTGAATAGTA ATGCCTGGAT GAACGACACT 1560  
GTCATAATTG ATAGTACAGT GGGAAAGGAC ACGTTCTTTC TCATCACATG GAACAGTCTG 1620  
CCTCCAGTA TTTCTCTCTG GGATCCCAGT GGAACAATAA TGGAAAATTT CACAGTGGAT 1680  
GCAACTTCCA AAATGGCCTA TCTCAGTATT CCAGGAACGT CAAAGGTGGG CACTTGGGCA 1740  
TACAATCTTC AAGCCAAAGC GAACCCAGAA ACATTAACTA TTACAGTAAC TTCTCGAGCA 1800  
GCAAATTCTT CTGTGCCTCC AATCACAGTG AATGCTAAAA TGAATAAGGA CGTAAACAGT 1860  
TTCCCCAGCC CAATGATTGT TTACGCAGAA ATTCTACAAG GATATGTACC TGTTCTTGGA 1920  
GCCAATGTGA CTGCTTCAT TGAATCACAG AATGGACATA CAGAAGTTTT GGAACCTTTG 1980  
GATAATGGTG CAGGCCTGA TTCTTCAGA AATGATGGAG TCTACTCCAG GTATTTACA 2040  
GCATATACAG AAAATGGCAG ATATAGCTTA AAAGTTCGGG CTCATGGAGG AGCAAACACT 2100  
GCCAGGCTAA AATTACGGCC TCCACTGAAT AGAGCCCGGT ACATACCAGG CTGGGTAGTG 2160  
AACGGGGAAA TTGAAGCAA CCCGCCAAGA CCTGAAATTG ATGAGGATAC TCAGACCACC 2220  
TTGGAGGATT TCAGCCGAAC AGCATCCCGA GGTGCATTTG TGTTATCACA AGTCCCAAGC 2280  
CTTCCCTTGC CTGACCAATA CCCACCAAGT CAAATCACAG ACCTTGATGC CACAGTTCAT 2340  
GAGGATAAGA TTATTCTTAC ATGGACAGCA CCAGGAGATA ATTTTGATGT TGAAAAGTT 2400  
CAACGTTATA TCATAAGAAT AAGTGCAAGT ATTCTTGATC TAAGAGACAG TTTTGATGAT 2460  
GCTCTTCAAG TAAATACTAC TGATCTGTCA CCAAAGGAGG CCAACTCCAA GGAAAGCTTT 2520  
GCATTTAAAC CAGAAAATAT CTCAGAAGAA AATGCAACCC ACATATTAT TGCCATTAAA 2580  
AGTATAGATA AAAGCAATTG GACATCAAA GTATCCAACA TTGCACAAGT AACTTTGTTT 2640  
ATCCCTCAAG CAAATCCTGA TGACATTGAT CCTACTCCTA CTCCTACTCC TACTCCTGAT 2700  
AAAAGTCATA ATTCTGGAGT TAATATTCT ACCTGGTAT TGTCTGTGAT TGGGTCTGTT 2760  
GTAATTGTTA ACTTTTTTT AAGTACCAAC CTTGAACCT TAACGAAGAA AAAATCTTC 2820  
AAGTAGACCT AGAAGAGAGT TTTAAAAAAC AAAACAATGT AAGTAAAGGA TATTCTGAA 2880  
TCTTAAATT CATCCCATGT GTGATCATAA ACTCATAAA ATAATTAA GATGTCGGAA 2940  
AAGGATACTT TGATTTAAATA AAAACACTCA TGGATATGTA AAAACTGTCA AGATTAAAAT 3000  
TTAATAGTTT CATTATTG TTATTTATT TGTAAGAAAT AGTGTGAAAC AAAGATCCTT 3060  
TTTCATACTG ATACCTGGTT GTATATTATT TGATGCAACA GTTTCTGAA ATGATATTTC 3120  
AAATTGCACTC AAGAAATTAA AATCATCTAT CTGAGTAGTC AAAATACAAG TAAAGGAGAG 3180  
CAAATAAACAA ACATTTGGAA AAAAAGGGAAA AAAAAGGGAAA

SEQ ID NO:34 Seq ID NO: 34 Protein sequence:

Protein Accession #: NP\_036260.1

1	11	21	31	41	51	
MGLFRGFVFL	LVLCLLHQSN	TSFIKLNNNNG	FEDIVIVIDP	SVPDEDEKIIE	QIEDMVTTAS	60
TYLFATEKR	FFFKNVSIL	PENWKENPQY	KRPKHENHKH	ADVIVAPPTL	PGRDEPYTKQ	120
FTECGEKGEY	IHFTPDLLL	KKQNEYGPPG	KLFVHEWAHL	RWGVFDEYNE	DQPFYRAKSK	180
KIEATRCSAG	ISGRNRVYKC	QGGSCLSRA	RIDSTTKLYG	KDCQFFPDKV	QTEKASIMFM	240
QSIDSVEFC	NEKTHNQEAP	SLQNIKCNFR	STWEVISNSE	DFKNTIPMVT	PPPPPVSLL	300
KIRQRIVCLV	LDKGSGSMGGK	DRLNRMNQAA	KHFLLQTVEN	GSWVGMVHFD	STATIVNKLI	360
QIKSSDERNT	LMAGLPTYPL	GGTSICSGIK	YAFQVIGELH	SQLDGSEVLL	LTDGEDNTAS	420
SCIDEVKQSG	AIVHFIALGR	AADEAVIEMS	KITGGSHFYV	SDEAQNNGLI	DAFGALTSGN	480
TDLSQKSQL	ESKGTLNSN	AWMNDTVIID	STVGKDFFL	ITWNSLPPSI	SLWDPSGTIM	540
ENFTVDATSK	MAYLSIPGTA	KVGTWAYNLQ	AKANPETLTI	TVTTSRAANSS	VPPITVNAKM	600
NKDVNSFPSP	MIVYAEILQG	YVPVLGANVT	AFIESQNQHT	EVLELLDNGA	GADSFKNNDGV	660
YSRYFTAYTE	NGRYSLKVR	HGGANTARLK	LRPPLNRAAY	IPGWVVNGEI	EANPPRPEID	720
EDTQTTLED	SRTASGGAFV	VSQVPSLPLP	DQYPPSQITD	LDATVHEDKI	ILTWTAPGDN	780
FDVGKVQRYI	IRISASILDL	RDSFDDALQV	NTTDLSPKEA	NSKESFAFKP	ENISEENATH	840
IFIAIKSIDK	SNLTSKVSNI	AQVTLFIPQA	NPDDIDPTPT	PTPTPDKSHN	SGVNISTLVL	900
SVIGSVVIVN	FILSTTI					

SEQ\_ID\_NO:35 Seq\_ID\_NO:35 DNA sequence  
Nucleic Acid Accession #: NM\_000901.1  
Coding sequence: 217-3171

1	11	21	31	41	51	
CGCGGGAGCC	AACTTCAGGC	TGCTCAGAGG	AAGCCCGTGC	AGTCAGTCAC	CTGGGTGCAA	60
GAGCGTTGCT	GCCTCGGGCT	CTCCCGCTGC	AGGGAGAGCG	GCACTCGCTG	GCCTGGATGT	120
GGTTGGATT	AGGGGGGCTC	CGCAGCAGGG	GTTTCGTGGC	GGTGGCAAGC	GCTGCAACAG	180
GTAGACGGCG	AGAGACGGAC	CCCAGGCGAG	GCAGGGATGG	AGACCAAAGG	CTACCACAGT	240
CTCCCTGAAG	GTCTAGATAT	GGAAAGACGG	TGGGGTCAAG	TTTCTCAGGC	TGTGGAGCGT	300
TCTTCCCTGG	GACCTACAGA	GAGGACCGAT	GAGAATAACT	ACATGGAGAT	TGTCAACGTA	360
AGCTGTGTT	CCGGTGCTAT	TCCAAACAAC	AGTACTCAAG	GAAGCAGCAA	AGAAAAAACAA	420
GAACTACTCC	CTTGCCTTCA	GCAAGACAAT	AATCGGCCCTG	GGATTTAAC	ATCTGATATT	480
AAAAGTGAGC	TGGAATCTAA	GGAACTTTCA	GCAACTGTAG	CTGAGTCCAT	GGGTTTATAT	540
ATGGATTCTG	TAAGAGATGC	TGACTATTCC	TATGAGCAGC	AGAACCAACA	AGGAAGCATG	600
AGTCCAGCTA	AGATTATATCA	GAATGTTGAA	CAGCTGGTGA	AATTTTACAA	AGGAAATGGC	660
CATCGTCCTT	CCACTCTAAG	TTGTGTGAAC	ACGCCCTG	GATCATTTAT	GTCTGACTCT	720
GGGAGCTCCG	TGAATGGTGG	CGTCATGCGC	GCCATTGTTA	AAAGCCCTAT	CATGTGTCAT	780
GAGAAAAGCC	CGTCTGTTG	CAGCCCTCTG	AAACATGACAT	CTTCGGTTG	CAGCCCTGCT	840
GGAATCAACT	CTGTGTCTC	CACCACAGCC	AGCTTGGCA	GTTCCTCAGT	GCACAGCCCC	900
ATCACCCAGG	GAACCTCCTCT	GACATGCTCC	CCTAATGCTG	AAAATCGAGG	CTCCAGGTG	960
CACAGCCCTG	CACATGCTAG	CAATGTGGC	TCTCCTCTCT	CAAGTCGTT	AAGTAGCATG	1020
AAATCCTCAA	TTTCCAGCCC	TCCAAGTCAC	TGCACTGTAA	AATCTCAGT	CTCCAGTCCC	1080
ATAATGTCA	CTCTGAGATC	CTCTGTGTC	AGCCTGCAA	ATATTAACAA	CTCAAGGTG	1140
TCTGTTCCA	GCCCTTCGAA	CACTAATAAC	AGATCCACGC	TTTCCAGTCC	GGCAGCCAGT	1200
ACTGTGGGAT	CTATCTGTAG	CCCTGTAAAC	AATGCCCTCA	GCTACACTGC	TTCTGGCACC	1260
TCTGCTGGAT	CCAGTACATT	GGGGGATGTG	GTTCCAGTC	CAGACACGCA	GGAGAAAGGT	1320
GCTCAAGAGG	TCCCTTTTCC	TAAGACTGAG	GAAGTAGAGA	GTGCCATCTC	AAATGGTGT	1380
ACTGGCCAGC	TTAATATTGT	CCAGTACATA	AAACCAGAAC	CAGATGGAGC	TTTTAGCAGC	1440
TCATGTCTAG	GAGGAAATAG	CAAAATAAT	TCGGATTCTT	CATTCTCAGT	ACCAATAAAG	1500
CAAGAATCAA	CCAAGCATT	ATGTTCAAGC	ACCTCTTTA	AAGGGAATCC	AACAGTAAAC	1560
CCGTTCCAT	TTATGGATGG	CTCGTATTT	TCCCTTATGG	ATGATAAAGA	CTATTATTCC	1620
CTATCAGGAA	TTTTAGGACC	ACCTGTGCC	GGCTTTGATG	GTAACTGTG	AGGCAGCGGA	1680
TTCCCAGTGG	GTATTAACAA	AGAACCCAGAT	GACGGGAGCT	ATTACCCAGA	GGCCAGCAGC	1740
CCTTCCTCTG	CTATTGTTGG	GGTGAATTCA	GGTGGACAGT	CCTTCCACTA	CAGGATTGGT	1800
GCTCAAGGTA	CAATATCTT	ATCACGATCG	GCTAGAGACC	AATCTTCCA	ACACCTGAGT	1860
TCCTTCCTC	CTGTCAAATAC	TTTAGTGGAG	TCATGGAAAT	CACACGGCGA	CCTGTCGTCT	1920
AGAAGAAGTG	ATGGGTATCC	GGTCTTAGAA	TACATTCCAG	AAAATGTATC	AAGCTCTACT	1980
TTACGAAGTG	TTTCTACTGG	ATCTTCAGA	CCTTCAAAAA	TATGTTGGT	GTGTGGGGAT	2040
GAGGCTTCAG	GATGCCATTA	TGGGGTAGTC	ACCTGTGGC	GCTGCAAAGT	TTTCTTCAA	2100
AGAGCAGTGG	AAGGGCAACA	CAACTATTTA	TGTGCTGGAA	GAAATGATTG	CATCATTGAT	2160
AAGATTGAC	GAAAGAATTG	TCCTGCTTC	AGACTTCAGA	AATGTTCTCA	AGCTGGAATG	2220
AATTAGGAG	CACGAAAGTC	AAAGAAGTTG	GGAAAGTTAA	AAGGGATTCA	CGAGGAGCAG	2280
CCACAGCAGC	AGCAGCCCC	ACCCCCACCC	CCACCCCCGC	AAAGCCCAGA	GGAGGGACA	2340
ACGTACATCG	CTCCTGCAA	AGAACCCCTG	GTCAACACAG	CACTGGTTCC	TCAGCTCTCC	2400
ACAATCTCAC	GAGGCTCAC	ACCTCCCC	GTTATGGTCC	TTGAAAACAT	TGAACCTGAA	2460
ATTGTATATG	CAGGCTATGA	CAGCTAAAAA	CCAGATACAG	CCGAAAATCT	GCTCTCCACG	2520
CTCAACCCTG	TAGCAGGCAA	ACAGATGATC	CAAGTCGTGA	AGTGGGCAA	GGTACTTCCA	2580
GGATTTAAA	ACTTGCCTCT	TGAGGACCAA	ATTACCCCTAA	TCCAGTATTG	TTGGATGTGT	2640
CTATCATCAT	TTGCCTTGAG	CTGGAGATCG	TACAAACATA	CGAACAGCCA	ATTTCCTCTAT	2700
TTTGCACCAAG	ACCTAGTCTT	TAATGAAGAG	AAGATGCATC	AGTCTGCCAT	GTATGAACTA	2760
TGCCAGGGGA	TGCACCAAAT	CAGCCTTCAG	TTCGTTCGAC	TGCAGCTCAC	CTTGTGAGAA	2820
TACACCATCA	TGAAAGTTT	GCTGCTACTA	AGCACAAATT	CAAAGGATGG	CCTCAAAAGC	2880
CAGGCTGCAT	TTGAAGAAAT	GAGGACAAAT	TACATCAAAG	AACTGAGGAA	GATGGTAACT	2940
AAAGTGTCCA	ACAATTCTGG	GCAGAGCTGG	CAGAGGTTCT	ACCAACTGAC	CAAGCTGCTG	3000
GACTCCATGC	ATGACCTGGT	GAGCGACCTG	CTGGAATTCT	GCTTCTACAC	CTTCCGAGAG	3060
TCCCAGTCGC	TGAAGGTAGA	GTTCCCCGCA	ATGCTGGTGG	AGATCATCAG	CGACCAGCTG	3120
CCCAAGGTGG	AGTGGGGAA	CGCCAAGCCG	CTCTACTTCC	ACCGGAAGTG	ACTGCCCCT	3180
GCCCAGAAGA	ACTTTGCCTT	AAGTTCCCT	GTGTTGTTCC	ACACCCAGAA	GGACCCAAGA	3240
AAACCTGTTT	TTAACATGTG	ATGGTTGATT	CACACTTGT	CAACAGTTTC	TCAAGTTAA	3300

AGTCATGTCA	GAGGTTTGG	GCCGGGAAAG	CTGTTTTCC	GTGGATTGG	CGAGACCAGA	3360
GCAGTCTGAA	GGATTCCCCA	CCTCCAATCC	CCCAGCGCTT	AGAAACATGT	TCCCTGTCCT	3420
CGGGATGAAA	AGCCATATCT	AGTCAATAAC	TCTGATTTG	ATATTTCAC	AGATGGAAGA	3480
AGTTTAACT	ATGCCGTGTA	GTTCCTGGTA	TCGTTCGCTT	GTTTTAAAAG	GGTTCAAGGA	3540
CTAACGAACG	TTTTAAAGCT	TACCCCTGGT	TTGCACATAA	AACGTATAGT	CAATATGGGG	3600
CATTAATATT	CTTTTGTAT	AAAAAAACA	AAAAAAATA	ATAAAAAAAT	ATATACAGAT	3660
TCCTGTTGT	TAATAACAGA	ACTCGTGGCG	TGGGGCAGCA	GCTGCCTCTG	AGCCCTCGCT	3720
CGTCCACGGT	CTTCTGCATC	ACTGGTATAC	ACACTCGTTA	GCGTCCATT	CTTATTTAAT	3780
TAGAATGGAT	AAGATGATGT	TAAATGCCTT	GGTTGATT	CTAGTATCTA	TTGTGTTGGC	3840
TTTACAAATA	ATTTTTGCA	GTCTTTGCT	GTGCTGTACA	TTACTGTATG	TATAAATTAT	3900
GAAGGACCTG	AAATAAGGT	TAAGGATCTT	TTGTAATGA	GACACATACA	AAAAAAATCT	3960
TTAATGGTTA	ATAGGATGAA	TGGGAAAGTA	TTTTGAAAG	AATTCTATT	TGCTGGAGAC	4020
TATTTAAGTA	CTATCTTGT	CTAAACAAGG	TAATTTTTT	TTGTAAGTG	CAATGTCCTG	4080
CATGCATAAT	GAACCGTTA	CAGTGTATT	AAGAAAGGGA	AAGCTGTGCC	TTTTTAGCT	4140
TCATATCTAA	TTTACCATTA	TTTACAGTC	TCTGTTGTAA	ATAACCACAC	TGAAACCTCT	4200
TCGGTTGTCT	TGAAACCTTT	CTACTTTTC	TGTACTTTT	GTGTTGTTCT	TGGTCTCCCG	4260
CTGGGGCAT	TTGTGGGACT	CCAGCACGTT	TTCTGGCTTC	TGCTTCATCC	TGCTCCATCG	4320
GGGAATGACA	CACTCGGGT	TCTGCAGCTC	CTGGAAGGTG	TCATTTGACA	ACACATGTGG	4380
GAGAGGAGGT	CCTTGGAGTG	CTGCAGCTT	GGGAAAGCCT	GCCTCGTTTC	CCTTTTCCTC	4440
TAGAAGCAGA	ACCAGCTCA	CGAGAGTGAN	ACTGGGAAC	TGATGGCTCA	GAGAGCATCT	4500
TTCCCTCCCA	TTTTAGAAAA	TCAGATTTC	TCCTGTGGGA	AAAAAAATT	CCATGCACTC	4560
TCTCTCTGTT	AAAGATCAGC	TATTCCCTTC	TGATCTTGG	AAGAGGTTCT	GCACCTCTGG	4620
AACCGGTAC	AGGAACGCAC	AGATCATGGC	AGGATGCGCT	GGGACGGCCC	ATCTTGGCAA	4680
GGTCAGTCT	GAATGGCATG	GAGACCGGG	GATAGAGGGG	TTTAGATTT	TTAAAGGTA	4740
GGTTTAA	ATAAGTTTA	TACATAAAC	GTGTTGGAGA	AAAATTACAG	ATCATATAAG	4800
CAAGACAGTG	GCAC	AAAT	TTAATCTGTT	TGTTTGGCAC	TGATGCAATG	4860
TATGGTTTT	CTCTGCCCC	AAATCACAAA	CATATGTATC	TTTGGGAAA	CTAACAAATAT	4920
GATTGCACTA	AATAAACTAC	TTGAAATAGA	GGCAAATT	ATCTTTAAA	AATGATGATA	4980
ATCATCAGGT	TTACTCAGT	AAATCATATT	AATTATTTT	CAAATCTAA	AAGCTGTAGC	5040
TGGAGAAGCC	CATGCCACG	AGGAAGCAGC	AATTAAATTAG	ATCAACACTT	TTCTCCAGGG	5100
TTCACCATGC	AGGCAACATT	ACCTTGTCTT	TCAAAGACA	CCTGCCTTAG	TGCAAGGGGA	5160
AACCTGTGAA	AGCTGCACTC	AGAGGGAGGA	GTCTTCTTA	CATAATTGC	AATTTCAGGA	5220
ATTTAATT	TAGGCAGATC	TTAAATACA	GTCAACTTAC	GGTGCACAGT	AATATGAAAG	5280
CCACACTTG	AAGGTAA	ATACACAGCA	TGCAGACTGG	GAGTTGCTAG	CAAACAAATG	5340
GCTTACTTAC	AAAAGCAGCT	TTTAGTTCA	ACTTAGTTT	TATAAAATGA	GAATTCTGAC	5400
TTACTTAACC	AGGTTTGGGA	TGGAGATGGT	CTGCATCAGC	TTTTGTATT	AACAAAGTTA	5460
CTGGCTCTT	GTGTGCTCC	AGGTAAC	GCTTGATTAA	ACAGCAAAGC	CATATTCTAA	5520
ATTCACTGTT	GAATGCCTGT	CCCAGTC	ATTGTCTGTC	TGCTCTTATT	TTGTACCAT	5580
ATTGCTCTTA	AAAATCTTGG	TTTGGTACAG	TTCATATT	ACCAAAAGT	TCATATAATT	5640
TAAAGAAACA	CTAAATTAGT	TTAAATGAA	GCAATTATA	TCTTTATGCA	AAAACATATG	5700
TCTGTCTTG	CAAAGGACTG	TAAGCAGATT	ACAATAAATC	CTTTACTTT		

SEQ ID NO:36 Seq ID NO: 36 Protein sequence:

Protein Accession #: NP\_000892.1

1	11	21	31	41	51	
METKGYHSLP	EGLDMERRWG	QVSQAVERSS	LGPTERTDEN	NYMEIVNVSC	VSGAIPNNST	60
QGSSKEKQEL	LPCLQQDNNR	PGILTSEDIKT	ELESKELSAT	VAESMGLYMD	SVRDADYSYE	120
QQNQQGSMSP	AKIYQNVEQL	VKFYKGNGHR	PSTLSCVNTP	LRSFMSDSGS	SVNGGVMRAl	180
VKSPIMCHEK	SPSVCSPLNM	TSSVCSPAGI	NSVSSTTASF	GSFPVHSPIT	QGTPLTCSPN	240
AENRGSRSHS	PAHASNVGSP	LSSPLSSMKS	SISSPPSHCS	VKSPVSSPNN	VTLRSSVSSP	300
ANINNSRCV	SSPSNTNNRS	TLSSPAASTV	GSICSPVNNA	FSYTASGTSA	GSSTLIRDVVP	360
SPDTQEKGQ	EVFPFKTEEV	ESAISNGVTG	QLNIVQYIKP	EPDGAFSSSC	LGGNNSKINS	420
SFSVPIKQE	STKHSCSGTS	FKGNPTVNP	PFMDGSYFSF	MDDKDYYSL	GILGPPVPGF	480
DGNCEGSGFP	VGIKQEPDDG	SYYPEASIPS	SAIVGVNSGG	QSFHYRIGAQ	GTISLSRSAR	540
DQS FQHLSSF	PPVNTLVESW	KSHGDLSSRR	SDGYPVLEYI	PENVSSSTLR	SVSTGSSRPS	600
KICLVCGDEA	SGCHYGVVTC	GSCKVFFKRA	VEGQHNYLCA	GRNDCIIDKI	RRKNCPACRL	660
QKCLQAGMNL	GARKSKKLGK	LKGIIHEEQPO	QQQPPPPPPP	PQSPEEGTTY	IAPAKEPSVN	720
TALVPQLSTI	SRALTPSPVM	VLENIEPEIV	YAGYDSSKPD	TAENLLSTLN	RLAGKQMIQV	780

VKWAKVLPGF KNLPLEDQIT LIQYSWMCLS SFALSWRSYK HTNSQFLYFA PDLVFNEEK	840
HQSAMYELCQ GMHQISLQFV RLQLTFEEYT IMKVLLLLST IPKDGLKSQA AFEEMRTNYI	900
KELRKMVTKC PNNSGQSWQR FYQLTKLLDS MHDLVSDLLE FCFYTFRESH ALKVEFPAML	960
VEIIISDQLPK VESGNAKPLY FHRK	

SEQ ID NO:37 Seq ID NO: 37 DNA sequence

Nucleic Acid Accession #: see Table 25 & 25A for complete list

1	11	21	31	41	51	
CCTACCAGGT	TCAAGCAACT	CTGCTGCCCT	AGCTCCCAAG	TAGCTGGAT	TACAGGTGCA	60
TGCCACTACA	CCTGGCTTTT	TGTATTTTTA	GTAGAGATGG	TTTTCACTAT	GTTGGCCAGG	120
CTGATCTTGA	ATTCTTGCC	TGAAGTAATC	TGCCTGCCCT	AGCCTCCAA	AGTGCTGGGA	180
TTATAGGAGC	CACCAACACCT	GGCATAACTG	GTATTTTTTA	TATGCTCCT	GGGCAACTTA	240
AAAAATTGAT	TACTCTGTTG	TTTCTTCCTT	TTTTTTTTT	TTTTGGCTTT	GACCAATTG	300
TGAGACCCAA	GTATCTCTA	CCTAGAAAAA	AAACACACTA	AACAGTAAAT	GATTACCAAC	360
CTATTTGGAA	CAAATCTAA	TTAATTAACA	TATACTTCAA	GGAGAAGACT	TAACAAAATC	420
TTACTTTCA	TTCTTAATAG	CTCTTCCAT	AAAAATGTTC	CACAAGTGT	TCAAATTAGT	480
CCTAACAACT	ACTGTTAAGT	GATTAATGAA	ACAGGAGTGA	CAGGAGTGA	TTAATAATA	540
GCAATAAATA	CAGATGGGAC	TACATAAATT	GTGGAGGTCC	TGATGCAAA	CTCTCTCTGT	600
ATTCGATGGC	ATCTCAGCTT	TCTCATAGAG	CTGTTTCACT	GTGAGGGTCT	TTATCCTTC	660
TGCAGAGCTT	CATTATTTTC	TTTCTTCAG	CAATCAGTCC	AAAGCACAA	GTCAGAAAGA	720
TCACAACACA	TGCAGCAATA	ATGGGCTCTA	TTGGTACACC	CACAGTTTA	TCTTTAACAA	780
TC						

SEQ ID NO:38 Seq ID NO: 38 DNA sequence

Nucleic Acid Accession #: NM\_001192.1

Coding sequence: 219-773

1	11	21	31	41	51	
AAGACTCAAA	CTTAGAAACT	TGAATTAGAT	GTGGTATTCA	AATCCTTACG	TGCCCGGAAG	60
ACACAGACAG	CCCCCGTAAG	AACCCACGAA	GCAGGGGAAG	TTCATTGTT	TCAACATTCT	120
AGCTGCTCTT	GCTGCATTG	CTCTGGAATT	CTTGTAGAGA	TATTACTTGT	CCTTCCAGGC	180
TGTTCTTCT	GTAGCTCCCT	TGTTTCTTT	TTGTGATCAT	GTTGCAGATG	GCTGGGCAGT	240
GCTCCAAAAA	TGAATATTTT	GACAGTTGT	TGCATGTTG	CATACCTTGT	CAACTTCGAT	300
GTTCTCTAA	TACTCCTCCT	CTAACATGTC	AGCGTTATTG	TAATGCAAGT	GTGACCAATT	360
CAGTGAAAGG	AACGAATGCG	ATTCTCTGGA	CCTGTTGGG	ACTGAGCTTA	ATAATTCTT	420
TGGCAGTTT	CGTGCTAATG	TTTTGCTAA	GGAAAGATAAG	CTCTGAACCA	TTAAAGGACG	480
AGTTTAAAAA	CACAGGATCA	GGTCTCCTGG	GCATGGCTAA	CATTGACCTG	AAAAGAGCA	540
GGACTGGTGA	TGAAATTATT	CTTCCGAGAG	GCCTCGAGTA	CACGGTGAA	GAATGCACCT	600
GTGAAGACTG	CATCAAGAGC	AAACCGAAGG	TCGACTCTGA	CCATTGCTTT	CCACTCCCAG	660
CTATGGAGGA	AGGGCAACC	ATTCTTGTC	CCACGAAAAC	GAATGACTAT	TGCAAGAGCC	720
TGCCAGCTGC	TTTGAGTGCT	ACGGAGATAG	AGAAAATCAAT	TTCTGCTAGG	TAATTAACCA	780
TTTCGACTCG	AGCAGTGCCA	CTTTAAAAAT	CTTTTGTCA	AATAGATGAT	GTGTCAGATC	840
TCTTTAGGAT	GACTGTATTT	TTCAAGTGCC	GATACAGCTT	TTTGTCTCT	AACTGTGGAA	900
ACTCTTTATG	TTAGATATAT	TTCTCTAGGT	TACTGTTGGG	AGCTTAATGG	TAGAAACTTC	960
CTTGGTTTCA	TGATTAAGT	CTTTTTTTT	CCTGA			

SEQ ID NO:39 Seq ID NO: 39 Protein sequence:

Protein Accession #: NP\_001183.1

1	11	21	31	41	51	
MLQMAGQCSQ	NEYFDSSLHA	CIPCQLRCSS	NTPPLTCQRY	CNASVTNSVK	GTNAILWTCL	60
GLSLIISLAV	FVLMFLLRKI	SSEPLKDEFK	NTGSGLLGMA	NIDLEKSRTG	DEIILPRGLE	120
YTVEECTCED	CIKSKPKVDS	DHCFPLPAME	EGATILVTTK	TNDYCKSLPA	ALSATEIEKS	180
ISAR						

SEQ ID NO:40 Seq ID NO: 40 DNA sequence  
 Nucleic Acid Accession #: NM\_025087.1  
 Coding sequence: 183-2282

1	11	21	31	41	51	
ACACTGCCTC	GGTTCGGCAA	GTGGGTCAGT	TGGCTGGGC	TCACCTGGCA	ACGGGACGCG	60
GGAACGAGGG	GCGCGGACGC	AGGCCCGGGA	GGACGCGCG	GCGGGAACCT	GGGGGCGCAG	120
GGCTAGGGCA	CGGGGCCGA	CCCGCACGGC	TTTCTGGAA	AGCGCTGCC	CTCGCCGCG	180
CGATGACCTC	GCTGTGGAGA	GAAATCCTCT	TGGAGTCGCT	GCTGGGATGT	TTTCTTGTT	240
CTCTCTACCA	TGACCTGGGA	CCGATGATCT	ATTACTTTCC	TTTGAAACA	CTAGAACTCA	300
CTGGGCTTGA	AGGTTTTAGT	ATAGCATTT	TTTCTCCAAT	ATTCTAACAA	ATTACTCCTT	360
TCTGGAAATT	GGTTAACAAAG	AAGTGGATGC	TAACCCTGCT	GAGGATAATC	ACTATTGGCA	420
GCATAGCCTC	CTTCCAGGCT	CCAAATGCCA	AACTTCGACT	GATGGTTCTT	GCGCTTGGGG	480
TGTCTTCCTC	ACTGATAGTG	CAAGCTGTGA	CTTGGTGGTC	AGGAAGTCAT	TTGCAAAGGT	540
ACCTCAGAAAT	TTGGGGATTTC	ATTTTAGGAC	AGATTGTTCT	TGTTGTTCTA	CGCATATGGT	600
ATACTTCACT	AAACCCAATC	TGGAGTTATC	AGATGTCCAA	CAAAGTGATA	CTGACATTAA	660
GTGCCATAGC	CACACTTGAT	CGTATTGGCA	CAGATGGTGA	CTGCAGTAAA	CCTGAAGAAA	720
AGAAGACTGG	TGAGGTAGCC	ACGGGGATGG	CCTCTAGACC	CAACTGGCTG	CTGGCAGGGG	780
CTGCTTTGG	TAGCCTTGTG	TTCCCTCACCC	ACTGGGTTTT	TGGAGAAGTC	TCTCTTGTT	840
CCAGATGGGC	AGTGAGTGGG	CATCCACATC	CAGGCCAGA	TCCTAACCCA	TTTGGAGGTG	900
CACTACTGCT	G TGCTTGCA	AGTGGATTGA	TGCTTCCATC	TTGTTTGTGG	TTTCGTGGTA	960
CTGGTTTGAT	CTGGTGGGTT	ACAGGAACAG	CTTCAGCTGC	GGGGCTCCTT	TACCTGCACA	1020
CATGGGCAGC	TGCTGTGTCT	GGCTGTGTCT	TCGCCATCTT	TACTGCATCC	ATGTGGCCCC	1080
AAACACTTGG	ACACCTTATT	AACTCAGGGA	CAAACCTGG	GAAAACATG	ACCATTGCCA	1140
TGATATTTTA	TCTTCTAGAA	ATATTTTCT	GTGCCTGGTG	CACAGCTTT	AAGTTTGTCC	1200
CAGGAGGTGT	CTACGCTAGA	GAAAGATCAG	ATGTGCTTTT	GGGGACAATG	ATGTTAATT	1260
TCGGGCTGAA	TATGCTATTT	GGTCCTAAGA	AAAACCTTGA	TTGCTCTT	AAACAAAAAA	1320
ACAGTTCTAA	AGTGTCTTTC	AGAAAGAGTG	AAAATACAT	GAAACTTTT	CTGTGGCTGC	1380
TTGTTGGTGT	GGGATTGTTG	GGATTAGGAC	TACGGCATAA	AGCCTATGAG	AGAAAACATGG	1440
GCAAAGTGGC	ACCAACAAA	GAGGTCTCTG	CTGCCATCTG	GCCTTCAGG	TTTGGATATG	1500
ACAATGAAGG	GTGGTCTAGT	CTAGAAAGAT	CAGCTCACCT	GCTCAATGAA	ACAGGTGCAG	1560
ATTTCATAAC	AATTTGGAG	AGTGATGCTT	CTAAGCCCTA	TATGGGAAAC	AATGACTTAA	1620
CCATGTGGCT	AGGGAAAAG	TTGGGTTCT	ATACAGACTT	TGGTCCAAGC	ACAAGGTATC	1680
ACACTGGGG	GATTATGGCT	TTGTCAAGAT	ACCCAATTGT	GAAATCTGAG	CATCACCTTC	1740
TTCCGTCAACC	AGAGGGCGAG	ATCGCACCA	CCATCACATT	GACCGTTAAC	ATTCGGGCA	1800
AGCTGGTGG	TTTTGTCGTG	ACACACTTG	GGAACACAGA	AGATGACCTC	GACAGGAAAC	1860
TGCAGGCTAT	TGCTGTTCA	AAACTACTGA	AAAGTAGCTC	TAATCAAGTG	ATATTTCTGG	1920
GATATATCAC	TTCAGCACCT	GGCTCCAGAG	ATTATCTACA	GCTCACTGAA	CATGGCAATG	1980
TGAAGGATAT	CGACAGCACT	GATCATGACA	GATGGTGTGA	ATACATTATG	TATCGAGGGC	2040
TGATCAGGTT	GGGTTATGCA	AGAATCTCCC	ATGCTGAACT	GAGTGATTCA	GAAATTCAAGA	2100
TGGCAAATT	TAGGATCCCT	GATGACCCCA	CTAATTATAG	AGACAACCAAG	AAAGTGGTCA	2160
TAGACCACAG	AGAAGTTCT	GAGAAAATTC	ATTTAATCC	CAGATTGGA	TCCTACAAAG	2220
AAGGACACAA	TTATGAAAAC	AACCATAATT	TTCATATGAA	TACTCCAAA	TACTTTTAT	2280
GAAACATTAA	AAACAAGAAG	TTATTGGCTG	GGAAAATCTA	AGAAAAAAAG	TATGTAAGAT	2340
AAAAAGAAGA	GATTAATGAA	AGTGGAAAAA	TACACATGAA	GAACCTAAC	TTAAAAAAC	2400
CATGGTATCT	ATGCAGTGGG	AAATTACCTC	CATTGTAAA	CTATGTTGCT	TAATAAAAAC	2460
ATTTCTCTAA	AAAAAAA	AAAAAA				

SEQ ID NO:41 Seq ID NO: 41 Protein sequence:  
 Protein Accession #: NP\_079363.1

1	11	21	31	41	51	
MTSLWREILL	ESLLGCVSWS	LYHDLGPMIY	YFPLQTLLELT	GLEGFSIAFL	SPIFLTITPF	60
WKLVNKKWML	TLLRIITIGS	IASFQAPNAK	LRLMVLALGV	SSSLIVQAVT	WWSGSHLQRY	120
LRIWGFILGQ	IVLVVLRIWY	TSLNPIWSYQ	MSNKVILTLS	AIATLDRIGT	DGDCKPKEK	180
KTGEVATGMA	SRPNWLLAGA	AFGSLVFLTH	WVFGEVSLVS	RWAVSGHPHP	GPDPNPFGGA	240
VLLCLASGLM	LPSCLWFRGT	GLIWWVTGTA	SAAGLLYLHT	WAAAASGCVF	AIFTASMWPQ	300
TLGHLINSGT	NPGKTMIAIM	IFYLLEIFFC	AWCTAFKFVP	GGVYARERSD	VLLGTMMLII	360

GLNMLFGPKK NLDLLLQTKN SSKVLFRKSE KYMKLFLWLL VGVGLLGLGL RHKAYERKLG 420  
KVAPTKEVSA AIWPFRFGYD NEGWLSSERS AHLLNNETGAD FITILESDAS KPYMGNNDLT 480  
MWLGEKLGFY TDFGPSTRYH TWGIMALSRY PIVKSEHHLL PSPEGEIAPA ITLTVNISGK 540  
LVDFVVTHFG NHEDDLDRKL QAIAVSKLLK SSSNQVIFLG YITSAPGSRD YLQLTEHGNV 600  
KDIDSTDHDR WCEYIMYRGL IRLGYARISH AELSDSEIQM AKFRIPDDPT NYRDNQKVVI 660  
DHREVSEKIH FNPRFGSYKE GHNYENNHNF HMNTPKYFL